

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 13:57:34 ; Search time 108.98 Seconds
(without alignments)
3741.440 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 4782
Sequence: 1 MKTSIPWLVSSVLAFSCHL.....MEIRGSSRNRYNDVGTKLR 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4782	100.0	928	2	AAW88417 Chlamydia
2	4782	100.0	928	3	AAAY90236 Chlamydia
3	4782	100.0	928	5	ABB90583 Chlamydia
4	4782	100.0	928	6	ABU26757 Protein e
5	4774	99.8	949	2	AAAY35060 Chlamydia
6	1862	38.9	918	3	AAAY69369 Amino aci
7	1855	38.8	928	3	AAAY94327 Chlamydia
8	1853	38.7	928	2	AAW88421 Chlamydia
9	1836	38.4	918	2	AAW88422 Chlamydia
10	1802	37.7	926	5	ABP56019 Chlamydia
11	1802	37.7	926	5	ABB98228 Chlamydia
12	1802	37.7	926	6	ABU6284 C. psitt
13	1794	37.5	928	5	ABB90542 Chlamydia
14	1794	37.5	928	9	ADW65028 C. pneumo
15	1793	37.5	928	2	AAW88423 Chlamydia
16	1787	37.4	928	3	AAAY90239 Chlamydia
17	1785	37.3	928	2	AAW88418 Chlamydia
18	1784	37.3	928	5	ABB90573 Chlamydia
19	1763	36.9	930	2	AAAY35052 Chlamydia
20	1761	36.8	930	5	ABB90548 Chlamydia
21	1761	36.8	930	6	ABU26756 Protein e
22	1758.5	36.7	927	6	AAAY3054 Chlamydia
23	1757	36.7	928	3	AAAY90237 Chlamydia
24	1755	36.7	930	2	AAW88424 Chlamydia

25	1755	36.7	930	3	AAAY90240 Chlamydia
26	1734	36.3	936	3	AAAY9842 Chlamydia
27	1734	36.3	936	5	ABB90602 Chlamydia
28	1734	36.3	936	6	ABU26755 Protein e
29	1732	36.2	914	2	AAW88429 Chlamydia
30	1705	35.7	925	3	AAAY9843 Chlamydia
31	1685	35.2	885	3	AAAY90238 Chlamydia
32	1634.5	34.2	945	3	AAAY9368 Mature Ch
33	1621.5	33.9	945	2	AAW88428 Amino aci
34	1562.5	32.7	839	5	ABP56002 Chlamydia
35	1562.5	32.7	839	5	ABB98211 Chlamydia
36	1562.5	32.7	839	6	ABU6287 C. psitt
37	1535	32.1	746	5	ABB90535 Chlamydia
38	1435.5	30.0	841	6	ABB90595 Chlamydia
39	1435.5	30.0	841	6	ABU26753 Protein e
40	1432.5	30.0	841	2	AAW88420 Chlamydia
41	1429.5	29.9	841	2	AAW88420 Chlamydia
42	1353	28.3	922	5	ABB90546 Chlamydia
43	1348	28.2	922	3	AAAY95548 Chlamydia
44	1345	28.1	922	2	AAAY34597 Chlamydia
45	1344	28.1	922	2	AAW88419 Chlamydia

ALIGNMENTS

RESULT 1
AAW88417
ID AAW88417 standard, protein, 928 AA.
XX
AC AAW88417;
XX
DT 17-OCT-2003 (revised)
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp4.
XX
KW Omp4, outer membrane protein 4; surface exposed protein; antigen; infection; diagnosis; vaccine; atheroclerosis; asthma.
XX
OS Chlamydia pneumoniae.
XX
PN W09858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK000266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHR/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
XX
DR WPI: 1999-105610/09.
DR N-PSDB; AAX06816.
XX
PT Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins.
XX
PS Claim 7; Page 40-42; 115pp; English.
XX
CC This polypeptide comprises the novel 98.9 kDa surface exposed protein Omp4 of the human respiratory pathogen Chlamydia pneumoniae. Its amino acid sequence was deduced from DNA (see AAX06816) isolated from a C. pneumoniae expression library. The invention provides 12 novel surface exposed proteins, Omp4-Omp15 (see AAX06816-27), and nucleic acid sequences encoding them (see AAX06816-27). A new species specific test is claimed that is used to identify mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer

membrane proteins, especially by PCR. The proteins are also used in the diagnosis of *C. pneumoniae* infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals. The nucleic acids being particularly useful as DNA vaccines for effecting *in vivo* expression of antigens. The vaccines may also prevent atherosclerosis and *C. pneumoniae* asthma, which are possibly associated with *C. pneumoniae*.
(Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 928 AA:

Query Match 100.0%; Score 4782; DB 2; Length 928;

Best Local Similarity 100.0%; Pred. No. 5.1e-307; Mismatches 0; Gaps 0;

Matches 928; Conservative 0; Indels 0; Gaps 0;

```

QY 1 MKTSIPWLVSSVAFSCNLSLNEELLSPDPSFNGIDSGFTPTPKTSATYSLTSDVF 60
DB 1 MKTSIPWLVSSVAFSCNLSLNEELLSPDPSFNGIDSGFTPTPKTSATYSLTSDVF 60
QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAASTTANKNLTFSGFS 120
DB 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAASTTANKNLTFSGFS 120
QY 121 LLSFDSSTPTVTGQGTLSAGGVNLENIRKLVVAGNFTADGAIKGAFLITGTSGD 180
DB 121 LLSFDSSTPTVTGQGTLSAGGVNLENIRKLVVAGNFTADGAIKGAFLITGTSGD 180
QY 121 LLSFDSSTPTVTGQGTLSAGGVNLENIRKLVVAGNFTADGAIKGAFLITGTSGD 180
DB 121 LLSFDSSTPTVTGQGTLSAGGVNLENIRKLVVAGNFTADGAIKGAFLITGTSGD 180
QY 181 ALFENNSSSTKGAIATTAGARINNTGYRFLNINASTSGAIDDEGTSLSNKFLYF 240
DB 181 ALFENNSSSTKGAIATTAGARINNTGYRFLNINASTSGAIDDEGTSLSNKFLYF 240
QY 241 EGNAAKTGTGAI CNTRKASGPELII SNKTLI PANSVAETSGAIIHAKKALSSGGFTPEP 300
DB 241 EGNAAKTGTGAI CNTRKASGPELII SNKTLI PANSVAETSGAIIHAKKALSSGGFTPEP 300
QY 241 EGNAAKTGTGAI CNTRKASGPELII SNKTLI PANSVAETSGAIIHAKKALSSGGFTPEP 300
DB 241 EGNAAKTGTGAI CNTRKASGPELII SNKTLI PANSVAETSGAIIHAKKALSSGGFTPEP 300
QY 301 LRRNVSSATPKGCAISIDAGSELBSAETGNITVRNLTITGSDTPPKRVAINIGSNGK 360
DB 301 LRRNVSSATPKGCAISIDAGSELBSAETGNITVRNLTITGSDTPPKRVAINIGSNGK 360
QY 361 FTELRAAKNHTIFFDPIITSEGTSSDVKINNAGALNPYQGTILFSGETLTDELKVA 420
DB 361 FTELRAAKNHTIFFDPIITSEGTSSDVKINNAGALNPYQGTILFSGETLTDELKVA 420
QY 421 DNLSKSFQPVSLSGCKLLQKGVTLBESTSFSEAGSLIGDMSGTTLSTAGSITITNLG 480
DB 421 DNLSKSFQPVSLSGCKLLQKGVTLBESTSFSEAGSLIGDMSGTTLSTAGSITITNLG 480
QY 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLANIDIEGNIYESHMSHDQLFSLKITYDAD 540
DB 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLANIDIEGNIYESHMSHDQLFSLKITYDAD 540
QY 541 VDTNVDISLLIPVPAEDPNSSEYFGQGNVMMTTDTATNTKEATYATWTKTGFVSPERKS 600
DB 541 VDTNVDISLLIPVPAEDPNSSEYFGQGNVMMTTDTATNTKEATYATWTKTGFVSPERKS 600
QY 601 ALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNFLAKTGDNENKGRHTISGG 660
DB 601 ALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNFLAKTGDNENKGRHTISGG 660
QY 661 VVIGGSATTPKDDLTFAFCHLPARDKOCFLAHNNSRYGGTLFKHSHTLOPQNYVRLG 720
DB 661 VVIGGSATTPKDDLTFAFCHLPARDKOCFLAHNNSRYGGTLFKHSHTLOPQNYVRLG 720
QY 721 RAKFESAEIAEKFPRIPLALDVQVFSHSDNRMEHTYSLPESBSWNECIAGIGIDL 780
DB 721 RAKFESAEIAEKFPRIPLALDVQVFSHSDNRMEHTYSLPESBSWNECIAGIGIDL 780
QY 781 PFLVSNPPLPFXFTIPLQKKEVNVVVSQNSPFESSSDGSGFISGRLLNLSIPVGAFFVGD 840
DB 781 PFLVSNPPLPFXFTIPLQKKEVNVVVSQNSPFESSSDGSGFISGRLLNLSIPVGAFFVGD 840
QY 841 IGDSTTYLDSGFVSDVYRNPNQSTATTVMSPDSWKIRGNSLRQAFLRGSNNVYNSN 900
DB 841 IGDSTTYLDSGFVSDVYRNPNQSTATTVMSPDSWKIRGNSLRQAFLRGSNNVYNSN 900

```

QY 901 CELFGHYAMELRGSSRNRYVDVGTKLRF 928
DB 901 CELFGHYAMELRGSSRNRYVDVGTKLRF 928

RESULT 2

AAV90236

ID AAV90236 standard; protein; 928 AA.

AC AAV90236;

DT 12-SEP-2003 (revised)

DT 29-AUG-2000 (first entry)

DE Chlamydia antigen CPN100634.

KM Chlamydia antigen; diagnosis; infection; community acquired pneumonia;

KW therapy; upper respiratory tract disease; bronchitis; sinusitis;

OS aethmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.

OS Chlamydia pneumoniae.

PN W0200032794-A2.

PD 08-JUN-2000.

PE 01-DEC-1999; 99MO-CA001147.

PR 01-DEC-1998; 98US-0110339P.

PR 01-DEC-1998; 98US-0110340P.

PR 01-DEC-1998; 98US-0110427P.

PR 01-DEC-1998; 98US-0110428P.

PR 01-DEC-1998; 98US-0110438P.

XX (CONN-) CONNAUGHT LAB LTD.

XX Murdin AD, Oomen RP, Wang J;

XX WPI: 2000-41239/35.

DR N-PSDB; AAA30847, AAA30848.

XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for

PT preventing, diagnosing and treating diseases such as community acquired

PT pneumonia, bronchitis, sinusitis and aethmatic bronchitis, adult-onset

PT asthma.

XX Claim 16; Fig 1; 174pp; English.

XX This sequence is a Chlamydia antigen of the invention, designated

CC CPN100634. The nucleic acids (and their complementary sequences) may be

CC used as diagnostic agents for detecting the presence of nucleic acids

CC encoding Chlamydia antigens in samples according to standard methods, and

CC therefore, for diagnosing Chlamydia infections. For example, they may be

CC used as primers and probes for diagnostic polymerase chain reaction (PCR)

CC assays. Antisense sequences may be used to down regulate expression of

CC the proteins and may be used to treat infections. The nucleic acids may

CC also be used to produce the protein antigens they encode according to

CC standard recombinant DNA methodologies. The proteins may then be used as

CC antigens for the production of antibodies (i.e. as vaccines) for

CC preventing infection by Chlamydia. The antibodies may also be used as

CC diagnostic reagents for detecting infections. Chlamydia is a pathogen

CC implicated in the development of (for example) community acquired

CC pneumonia, upper respiratory tract disease (especially bronchitis and

CC sinusitis, aethmatic bronchitis, adult-onset asthma and acute

CC exacerbations of asthma in adults. (Updated on 12-SEP-2003 to standardise

CC OS field)

XX Sequence 928 AA:

Query Match 100.0%; Score 4782; DB 3; Length 928;
Best Local Similarity 100.0%; Pred. No. 5.1e-307; Mismatches 0; Gaps 0;
Matches 928; Conservative 0; Indels 0; Gaps 0;

```

QY 1 MKTSLPWLVSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFPTPKTSATTYSLTGDFV 60
DB 1 MKTSLPWLVSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFPTPKTSATTYSLTGDFV 60
QY 61 FYRPGKCTPLSDSCFKOTDNLTFLLNGHSLTGFIDAGTHAGAASTYANKULTRSGFS 120
DB 61 FYRPGKCTPLSDSCFKOTDNLTFLLNGHSLTGFIDAGTHAGAASTYANKULTRSGFS 120
QY 121 LLSFDDSPSTVTYTGQGLSSAGVNLNIRKLVAGNFSTAGGAIKGSFLLTGSGD 180
DB 121 LLSFDDSPSTVTYTGQGLSSAGVNLNIRKLVAGNFSTAGGAIKGSFLLTGSGD 180
QY 181 ALFSNNSSSTKGGAIAATTAGARIANNTRYRPLSNLSTSGAIDDEGTSILSNKFLYF 240
DB 181 ALFSNNSSSTKGGAIAATTAGARIANNTRYRPLSNLSTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTGGAIQNTYKASGSPPELLISNNKTLIPASNAVETSGAIIHAKKULALSSGFTF 300
DB 241 EGNAAKTGGAIQNTYKASGSPPELLISNNKTLIPASNAVETSGAIIHAKKULALSSGFTF 300
QY 301 LRNNSSATPKGAISTDASGELSLAETGNITFVRNTLTITTSSTDPKRNAINISNGK 360
DB 301 LRNNSSATPKGAISTDASGELSLAETGNITFVRNTLTITTSSTDPKRNAINISNGK 360
QY 361 FTFLRAAKNTTIFFYDPTTSEGTSDVLKINNAGALANFYOGTILFSGETTLADELKYA 420
DB 361 FTFLRAAKNTTIFFYDPTTSEGTSDVLKINNAGALANFYOGTILFSGETTLADELKYA 420
QY 421 DNKSSFTQPVSLGGKLLIQKVLTSTSPSOEAGSLGMDSGTLLSTAGSITTTNIG 480
DB 421 DNKSSFTQPVSLGGKLLIQKVLTSTSPSOEAGSLGMDSGTLLSTAGSITTTNIG 480
QY 481 INVDSLGLQPVSLTAKGANKYIVSGKLLIDEGIVESHMFSDQLFSLKITVDDAD 540
DB 481 INVDSLGLQPVSLTAKGANKYIVSGKLLIDEGIVESHMFSDQLFSLKITVDDAD 540
QY 541 VDTNVISSLIIPPAEDPNSEYFGQGMVNTTDTATNTKEATYATWTKGFPVSPERKS 600
DB 541 VDTNVISSLIIPPAEDPNSEYFGQGMVNTTDTATNTKEATYATWTKGFPVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNPLAKTGDENRKCFRHTSG 660
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNPLAKTGDENRKCFRHTSG 660
QY 661 YVIGGSANFTPKDULFTFAFCHLPARDKCFIAHNSRTYGTLPFKKSHLQONTLRIG 720
DB 661 YVIGGSANFTPKDULFTFAFCHLPARDKCFIAHNSRTYGTLPFKKSHLQONTLRIG 720
QY 721 RAKFSASAIKFPREIPLALDOVVSFSDNRMEHTYSLPESGGSNSNCIAGGIGLGL 780
DB 721 RAKFSASAIKFPREIPLALDOVVSFSDNRMEHTYSLPESGGSNSNCIAGGIGLGL 780
QY 781 PVLNSNPHELEKFTIPOMKVEVMYVSONSFESSSDGRGFSIRLLNLSIPVAKFVOGD 840
DB 781 PVLNSNPHELEKFTIPOMKVEVMYVSONSFESSSDGRGFSIRLLNLSIPVAKFVOGD 840
QY 841 IGSYTYDLSGFVSDVYRNNPOSTATLVMSPSWKIRGNLSROAFLRGSNNYYNSN 900
DB 841 IGSYTYDLSGFVSDVYRNNPOSTATLVMSPSWKIRGNLSROAFLRGSNNYYNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTKLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTKLRF 928

```

```

DT 29-JUL-2002 (first entry)
XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
DE Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
KW Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CWL029.
XX Chlamydia pneumoniae.
OS Chlamydia pneumoniae.
XX Chlamydia pneumoniae.
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein /label= Signal_peptide
FT 18..928
FT /note= "mature protein"
XX MO200202606-A2.
XX 10-JAN-2002.
PD 03-JUL-2001; 2001WC-IB001445.
XX 03-JUL-2000; 2000GB-00016363.
XX 11-JUL-2000; 2000GB-00017047.
XX 21-JUL-2000; 2000GB-00017983.
XX 07-AUG-2000; 2000GB-00019368.
XX 18-AUG-2000; 2000GB-00020440.
XX 14-SEP-2000; 2000GB-00022583.
XX 10-NOV-2000; 2000GB-00027549.
XX 22-DEC-2000; 2000GB-00031706.
XX (CHIR-) CHIRON SPA.
XX Ratti G, Grandi G;
XX N-PSDB; ABL91241.
XX WPI; 2002-154726/20.
DR Chlamydia pneumoniae protein useful in the manufacture of a
XX novel Chlamydia pneumoniae protein useful in the manufacture of a
XX medicament for treatment or prevention of infection due to Chlamydia,
XX preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX Claim 1; Page 96-97; 364pp; English.
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
XX pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
XX them. The proteins are predicted to be immunogenic and may therefore be
XX useful in vaccine production and for diagnostic purposes. Chlamydia
XX pneumoniae is a common cause of respiratory disease in humans, and is
XX also involved in the development of cardiovascular diseases such as
XX atherosclerosis, coronary artery disease, carotid artery stenosis,
XX myocardial infarction, cerebrovascular disease, aortic aneurysm,
XX claudication and stroke. The proteins and nucleic acids of the invention
XX may be used in vaccines and pharmaceutical compositions for the
XX prevention or treatment of chlamydial infections, particularly Chlamydia
XX pneumoniae infections. The proteins may also be used in the detection of
XX Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
XX DNA probe assay or blotting techniques for determining Chlamydia
XX pneumoniae gene expression. The present sequence represents a
XX specifically claimed Chlamydia pneumoniae protein of the invention.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 928 AA:
Query Match 100.0%; Score 4782; DB 5; Length 928;
Best local similarity 100.0%; Pred. No. 5.1e-307;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTSLPWLVSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFPTPKTSATTYSLTGDFV 60
DB 1 MKTSLPWLVSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFPTPKTSATTYSLTGDFV 60

```

```

QY 61 FVEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGLDAGTHAGAASTTANKNLTSGFS 120
DB 61 FVEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGLDAGTHAGAASTTANKNLTSGFS 120
QY 121 LLSFDSSPSTTTVTTCGTSSAGVNLNIRKLVVAGNESTADGAIKGAFLITGSGD 180
DB 121 LLSFDSSPSTTTVTTCGTSSAGVNLNIRKLVVAGNESTADGAIKGAFLITGSGD 180
QY 181 ALFSNNSSSTKGAIAATTAGARIANNNGYRPLSNLTASTSGAIDDEGSIILSNKFLYF 240
DB 181 ALFSNNSSSTKGAIAATTAGARIANNNGYRPLSNLTASTSGAIDDEGSIILSNKFLYF 240
QY 241 EGNAAKTTGCAICNTKASGSPILLISNNKTLIFASNAVETSGGAIHAKKALALSSGFTTF 300
DB 241 EGNAAKTTGCAICNTKASGSPILLISNNKTLIFASNAVETSGGAIHAKKALALSSGFTTF 300
QY 301 LRNNVSATPKGGAISIDASGELSLETGNITFVRNTLTGSGTDPKRNAINIGSNGK 360
DB 301 LRNNVSATPKGGAISIDASGELSLETGNITFVRNTLTGSGTDPKRNAINIGSNGK 360
QY 361 FTELRAKNNHTTFYDPTSEGTSDVLKINNAGALNFPYQGITLPSGETLADDELKVA 420
DB 361 FTELRAKNNHTTFYDPTSEGTSDVLKINNAGALNFPYQGITLPSGETLADDELKVA 420
QY 421 DNLSKSFQPVSLSGGKLLQKGVLTSTSPSOAGSLLGWDSGTTLTAGSITITNLG 480
DB 421 DNLSKSFQPVSLSGGKLLQKGVLTSTSPSOAGSLLGWDSGTTLTAGSITITNLG 480
QY 481 INVDSLGLKOPVSLTAKGASNKVIVSGKLNIDIEGNIYESHMSHDLQFLSKITVDAD 540
DB 481 INVDSLGLKOPVSLTAKGASNKVIVSGKLNIDIEGNIYESHMSHDLQFLSKITVDAD 540
QY 541 VDTNVDISLILPVAEDPNSYEGOGQNNVMTDTATNKEATATYTKTGVPSPERKS 600
DB 541 VDTNVDISLILPVAEDPNSYEGOGQNNVMTDTATNKEATATYTKTGVPSPERKS 600
QY 601 ALVNCNTMGVFTDTRSLQQLVEIGATGMEHKGFVWSSMTNLFHKTDENRKGFRTSGG 660
DB 601 ALVNCNTMGVFTDTRSLQQLVEIGATGMEHKGFVWSSMTNLFHKTDENRKGFRTSGG 660
QY 661 YVIGGSAHTPKDIDFTFAFCHLPARDKOCFIANNHSTYGGTLEFKKSHITLQPNYLRG 720
DB 661 YVIGGSAHTPKDIDFTFAFCHLPARDKOCFIANNHSTYGGTLEFKKSHITLQPNYLRG 720
QY 721 RAKSESASIEKPEPEIPLADVVSFSHSDRMETHHTSLPESGSMNECTIAGIGIDL 780
DB 721 RAKSESASIEKPEPEIPLADVVSFSHSDRMETHHTSLPESGSMNECTIAGIGIDL 780
QY 781 PFVLSNPPLFKTFIPQMKVEMVYVVSQNSPFSSSDGRGFSIGRLNLIPVGAKEVQGD 840
DB 781 PFVLSNPPLFKTFIPQMKVEMVYVVSQNSPFSSSDGRGFSIGRLNLIPVGAKEVQGD 840
QY 841 IGDSTYVDLSGFPVSDVYRNNPOSTATILVMSPDWKIRGNLSRQAFILRGSNNYVYNSN 900
DB 841 IGDSTYVDLSGFPVSDVYRNNPOSTATILVMSPDWKIRGNLSRQAFILRGSNNYVYNSN 900
QY 901 CELFGHYAMELRGSSRRNNVUGTKLRF 928
DB 901 CELFGHYAMELRGSSRRNNVUGTKLRF 928

```

RESULT 4
ABU26757 standard; protein, 928 AA.

ABU26757;

23-OCT-2003 (revised)
19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #12284.

```

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Chlamydomonada pneumoniae.
XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342823P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KU, Zykind JW,
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX WPI: 2003-029926/02.
XX N-PSDB; ACA30627.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 54681; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 928 AA:
XX
XX Query Match 100.0%; Score 4782; DB 6; Length 928;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-307; Indels 0; Gaps 0;
XX Matches 928; Conservative 0; Mismatches 0;
QY 1 MKTISIPWLVSSVLAFCCHLOSLANEELSLPDDSFNGNINSGFTPTKTSATYSLTGVDF 60
DB 1 MKTISIPWLVSSVLAFCCHLOSLANEELSLPDDSFNGNINSGFTPTKTSATYSLTGVDF 60

```



```

QY 61 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTANKULTFSGFS 120
Db 61 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTANKULTFSGFS 120
QY 121 LLSFDSSTPTVTTGQGTLSAGGVNLENIRKLVVAGNFTAGGAIKKAFLTLTSGD 180
Db 121 LLSFDSSTPTVTTGQGTLSAGGVNLENIRKLVVAGNFTAGGAIKKAFLTLTSGD 180
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
Db 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTGGAI CNTRKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASGGFTTF 300
Db 241 EGNAAKTGGAI CNTRKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASGGFTTF 300
QY 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
Db 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
QY 361 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINNSAGALNPYOGTILFSGETTLADELKVA 420
Db 361 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINNSAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNLKSSFTQPVSLSGGKLLQKGVLTBSTSPSQEAGSLGMDSGTTLSTTAGSITITNLG 480
Db 421 DNLKSSFTQPVSLSGGKLLQKGVLTBSTSPSQEAGSLGMDSGTTLSTTAGSITITNLG 480
QY 481 INVDISLGLKQPVSLTAKGASNKIVSGKLLIDIEGVIYSHMFSHQFLSLKITVYDAD 540
Db 481 INVDISLGLKQPVSLTAKGASNKIVSGKLLIDIEGVIYSHMFSHQFLSLKITVYDAD 540
QY 541 VDTNVDISLIPPAEDPNSEYGFQGGOMVNMWTTDTATNKREATAWTGKGFVPSPERKS 600
Db 541 VDTNVDISLIPPAEDPNSEYGFQGGOMVNMWTTDTATNKREATAWTGKGFVPSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWVSMNPLHKTGDENRKGFRHTSGG 660
Db 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWVSMNPLHKTGDENRKGFRHTSGG 660
QY 661 YVIGGSATHTPKDULFFPAFCHLFAKDCCTIAHNSSTYGGTLFPKASHLQONTYLRIG 720
Db 661 YVIGGSATHTPKDULFFPAFCHLFAKDCCTIAHNSSTYGGTLFPKASHLQONTYLRIG 720
QY 721 RAKFSSEAIKPREIPLALDVQVFSHSDNRMEHTYSLPESGSMNSNCIAGIGLGL 780
Db 721 RAKFSSEAIKPREIPLALDVQVFSHSDNRMEHTYSLPESGSMNSNCIAGIGLGL 780
QY 781 PVLASNPHLPFKTFIPQMKVEMYVVSQNSFFESSSDGRGFSIGRLNLSIPVAKFVQGD 840
Db 781 PVLASNPHLPFKTFIPQMKVEMYVVSQNSFFESSSDGRGFSIGRLNLSIPVAKFVQGD 840
QY 841 IGSSTYDLSGFRVSDVYRNNPOSTATLVMSPDWKTREGNLSROAFLRGSNNYYNSN 900
Db 841 IGSSTYDLSGFRVSDVYRNNPOSTATLVMSPDWKTREGNLSROAFLRGSNNYYNSN 900
QY 901 CELFGHYAMELRGSSRRYNDVGTCLRF 928
Db 901 CELFGHYAMELRGSSRRYNDVGTCLRF 928

```

```

KW sinuetis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope.
OS Chlamydia pneumoniae.
PN MO9927105-A2.
XX 03-JUN-1999.
PD
PF 20-NOV-1998; 98MO-1B001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT
PS Page 947-949; Disclosure; 1912pp; English.
XX
CC AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 949 AA;
Query Match 99.8%; Score 4774; DB 2; Length 949;
Best Local Similarity 99.9%; Pred. No. 1.8e-306;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKTSLPVLVSVLAFSCHLQSLANBELLPDPSFNGNIDSGTFPKTSATYSLTGDF 60
Db 22 MKTSLPVLVSVLAFSCHLQSLANBELLPDPSFNGNIDSGTFPKTSATYSLTGDF 81
QY 61 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTANKULTFSGFS 120
Db 82 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTANKULTFSGFS 141
QY 121 LLSFDSSTPTVTTGQGTLSAGGVNLENIRKLVVAGNFTAGGAIKKAFLTLTSGD 180
Db 142 LLSFDSSTPTVTTGQGTLSAGGVNLENIRKLVVAGNFTAGGAIKKAFLTLTSGD 201
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
Db 202 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 261
QY 241 EGNAAKTGGAI CNTRKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASGGFTTF 300
Db 262 EGNAAKTGGAI CNTRKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASGGFTTF 321
QY 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
Db 322 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 381
QY 361 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINNSAGALNPYOGTILFSGETTLADELKVA 420
Db 382 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINNSAGALNPYOGTILFSGETTLADELKVA 441
QY 421 DNLKSSFTQPVSLSGGKLLQKGVLTBSTSPSQEAGSLGMDSGTTLSTTAGSITITNLG 480
Db 442 DNLKSSFTQPVSLSGGKLLQKGVLTBSTSPSQEAGSLGMDSGTTLSTTAGSITITNLG 501

```

QY 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNIDIEGNIYESHMFSDQLFSLKITVDAD 540
XX |||||
Db 502 INVDSLGLKQPVSLTAKGASNKVIVSGKLNIDIEGNIYESHMFSDQLFSLKITVDAD 561
QY 541 VDTNVDISLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATVTKTGFVPSPERKS 600
XX |||||
Db 562 VDTNVDISLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATVTKTGFVPSPERKS 621
QY 601 ALVNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSMTNFKLTKGTDENRKGFRHTSGG 660
XX |||||
Db 622 ALVNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSMTNFKLTKGTDENRKGFRHTSGG 681
QY 661 YVIGSAAHPKDDLTFAFCHLFAKDQCFIAHNNSRITYGTLTFKSHHTLQPNYLRIG 720
XX |||||
Db 682 YVIGSAAHPKDDLTFAFCHLFAKDQCFIAHNNSRITYGTLTFKSHHTLQPNYLRIG 741
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSHSDNRMTHTYSLPESGGSNNECIAIGIGLDL 780
XX |||||
Db 742 RAKFSESAIEKFPREIPLALDVQVSFSHSDNRMTHTYSLPESGGSNNECIAIGIGLDL 801
QY 781 PFVLSNPHPLFKFTIPQMKVEMVYVVSQNSPFESSDDGRGFSIGRLNLSIPVGAKEVQGD 840
XX |||||
Db 802 PFVLSNPHPLFKFTIPQMKVEMVYVVSQNSPFESSDDGRGFSIGRLNLSIPVGAKEVQGD 861
QY 841 IGDSTYDLSGFPVSDVYRNNDPOSTATLVMSPDMSKIRGNIISRQAFLLRGSNNYVNSN 900
XX |||||
Db 862 IGDSTYDLSGFPVSDVYRNNDPOSTATLVMSPDMSKIRGNIISRQAFLLRGSNNYVNSN 921
QY 901 CELFGHYAMELRGSSRNRYNDVGTKLRF 928
XX |||||
Db 922 CELFGHYAMELRGSSRNRYNDVGTKLRF 949

RESULT 6

AA69369 standard; protein; 918 AA.

AA69369;

12-SEP-2003 (revised)

19-JUN-2000 (first entry)

Amino acid sequence of the CPN100395 polypeptide.

CPN100395; Chlamydia infection; immune response; vaccine.

Chlamydia pneumoniae.

MO20001183-A2.

02-MAR-2000.

18-AUG-1999; 99WO-1B001449.

20-AUG-1998; 98US-0097187P.

20-AUG-1998; 98US-0097188P.

20-AUG-1998; 98US-0097189P.

20-AUG-1998; 98US-0097190P.

20-AUG-1998; 98US-0097195P.

20-AUG-1998; 98US-0097196P.

20-AUG-1998; 98US-0097197P.

27-AUG-1998; 98US-0097191P.

17-AUG-1999; 99US-00376770.

(CONN-) CONNNAUGHT LAB LTD.

Muridin AD, Oomen RP;

WPI; 2000-224703/19.

N-PSDB; AAZ61509.

Novel antigens and corresponding DNA molecules that can be used to

PT prevent, treat and diagnose disease caused by Chlamydia infection in
PT mammals, especially humans.

PS Claim 19; Fig 15-E; 201p; English.

XX AA69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides
CC are present in the bacterial membrane structure, in the external vicinity
CC of the membrane structure, in the inclusion membrane structure, in the
CC external vicinity of the inclusion membrane structure, and in the
CC cytoplasm of the infected cell. The polypeptides may be used to prevent,
CC treat and detect the presence of Chlamydia infection and/or the presence
CC of Chlamydia in a sample. The polypeptides may also be used to induce an
CC immune response in a mammal. The vaccine vector comprising the
CC polynucleotides is used to induce an immune response in a mammal.
CC Antibodies directed against the polypeptides may also be used
CC therapeutically to treat and/or prevent a Chlamydia infection. (Updated
CC on 12-SEP-2003 to standardise OS field)

XX Sequence 918 AA;

SQ Query Match 38.9%; Score 1862; DB 3; Length 918;

Best Local Similarity 42.3%; Pred. No. 4, 9e-114;

Matches 398; Conservative 156; Mismatches 352; Indels 34; Gaps 12;

QY 1 MKTSLPWLVSVALAFSCHLQSL---ANBELSPDPSFNGNIDSGFTTPK-----TSATT 52

Db 1 MRSSFSLLTSSSLAEPPL-LMSVSADAADLTLSRDSYNDGTSFTTEFPKATSDASGAT 59

QY 53 YSLTGVFFPEPKGPIPLSDSCFKOTTDNLTFIGNHSLTFPGTIDGTNAGAASTTANK 112

Db 60 YILDGVVISQAKQOTSLTTSFCSNTRAGNLFIGNFSLFDNIISTYAGVVSNTAAS 119

QY 113 NLT-FSGFSLSPDSSPTVTVTGOTLSAGGVNLENIKLVAAGFSTADGAIKAS 171

Db 120 GITKFSGFSLTMLAAPR---TTGKAIKITDGLVESIGNLNLNENASENGALINTKT 176

QY 172 FLITGTSGDALEFNNSSSTYGAIATTAGKRIANNTRYRFLSNISTSGAIDDEGTSI 231

Db 177 LSLTGSTRFVAFPLGNSSQCGAIVASGDSVISENAGILSFGNNSATYSGGAIASAGNVL 236

QY 232 LSNNKFLYFEGNAKTTGAIICNTKASGPE--LIISNNKTLFASVARETSAGAIHAKK 289

Db 237 ISNNQNIFFDGCATTTGGAIDCNKAGANDPILTLISGNSLHFLNNTAENSAGAIYTKK 296

QY 290 LALSQG-GTFEFLRNWVSATPKGAISIDAGELSLAETGNIITFVRNTLTGTSDDTP 348

Db 297 LIVLSGKGVLFENNAANATPKGAIALIDSEGISADLGNIIPEGNTTSTGSPASV 356

QY 349 KRNAINIGSNGKTELRPAKNHTIFPYDPTTSGTSSDVLIKNNAGALNPYOGTILFS 408

Db 357 TRNAIDLASNAKFLNTRATGNKVIFPYDPTSSG-ATDKLSLNKADAGSGNTTEGYIVFS 415

QY 409 GETLTDELKVADNLKSFOTPOVSLSGGKLLKGVTLESTSPQASGLLGDGSTTLS 468

Db 416 GEKLSBELKKPDVLASTFTQAVELAGALVLKQGVTVANTTTQVEGSKVYMDGGTTFE 475

QY 469 TTGASITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNIDIEGNIYESHMFSDQ 528

Db 476 ASAEGVTLNGLAINISLDGNTKAIIKATGASDVALSGLIMLVDAQNYEHNHNSQQQ 535

QY 529 LFSLLKTTVDADVDTNVDISLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATVTK 588

Db 536 VFPLIEISAOGTM-TTVDIPD---TPLINTNNHYGQGMNINIVWDATKATKNAALTLWT 591

QY 589 KTGFPVSPERKSLALVCTLWGVFTDIRSLQQLVEIGATGMEHKQGFVWSMTNFKLTKGT 648

Db 592 KTGKPNPERQGPLVPSLWGSFVDSIQSLMDRSTSSLSSTNMLVSGIADFLYHEDOK 651

QY 649 ENRKGFRHTSGGVYIGGSAHTPKDCLTFPAFCHLFAKDQCFIAHNNSRITYGTLTFPKHS 708

Db 652 GNGRSYHSSAGTALGGFFTTASBNFNFACQLFGVDXOHLVAKNHTHYAAGMSYRH- 710

QY 709 HTLOPQNYLRLGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMTHTYSLPESGGSWS 768

PR 23-JUN-1997; 97DK-00000744.
XX (BIRK/) BIRKELUND S.
PA (CHR/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P,
XX WPI; 1999-105610/09.
DR N-PSDB; AAX06821.
XX
PT Species-specific test for identifying mammals infected with Chlamydia
PT pneumoniae - comprises detecting antibodies specific for outer membrane
PT proteins of C. pneumoniae or nucleic acids encoding these proteins.
XX
PS Claim 7; Page 56-58; 115pp; English.
XX
CC This polypeptide comprises the novel 96.7 kDa surface exposed protein
CC Omp5 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
CC acid sequence was deduced from DNA (see AAX06821) isolated from a C.
CC pneumoniae expression library. The invention provides 12 novel surface
CC exposed proteins, Omp4-Omp15 (see AAX068417-28), and nucleic acid
CC sequences encoding them (see AAX06816-27). A new species specific test is
CC claimed that is used to identify mammals (including humans) infected with
CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
CC proteins can also be used in the immunization of mammals, the nucleic
CC acids being particularly useful as DNA vaccines for effecting in vivo
CC expression of antigens. The vaccines may also prevent atherosclerosis and
CC bronchial asthma, which are possibly associated with C. pneumoniae.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 918 AA:

Query Match 38.4%; Score 1836; DB 2; Length 918;
Best Local Similarity 42.1%; Pred. No. 2.6e-112;
Matches 396; Conservative 155; Mismatches 355; Indels 34; Gaps 12;

QY 1 MKTSIPWVVSVLAFSCHQSL--ANEELSPDDSFNNGNDSGTPRK-----TSAT 52
DB 1 MRSSFSLLISSSLAFPL-LMSVADADADLTLSRDSYNDSTETETPPAATSDDASGTT 59
QY 53 YSLTGDFEYEPKGTPLSDSCFQQTNDLTFLLNGHSLTFEGFDAGTHAAGAATSTANK 112
DB 60 YIIDGVISIQAGKQTLTSCBSNTAGNLTFLLNGSLFNDIISTVAGVVSNTAAS 119
QY 113 NLTF-FSGFSLSPDSPTVTGQGTLSAGGVNLEIRKLVAAGNFSTADGAIKAS 171
DB 120 GITKFSGFSTLRMLAAR--TTGKGAIKITDGLVFESIGNLDQNEAASSENGCAINTKT 176
QY 172 FLUTGTSGDALFSSNNSSTGTGAIAATTAGARIANTGYVFLNSIASTSGAIDDEGTST 231
DB 177 LSLTGSTRFAVFLGNSSSQGGAIVAGDVISNNAIILFPGNNSAATTSAGAISAEENLV 236
QY 232 LSNKKFLYFEGNAKTGGAICMTKASGPE--LIISNNKTLFASVVAETSGGAIHAKK 289
DB 237 ISNNQITFFPGCAATTGGAIDCKKAGANPDITLISGNSLHFLNNTAGNSGGAITYKK 296
QY 290 LALSSG-GFTEPLRNNVSATPKGAISIDASGELSLAETGNITFVRNTLTGSTDTP 348
DB 297 LVLSGSGGVLFSSNKAANTPKGAIATLDSGELISADLGNITFEAGNTSTTSGPASV 356
QY 349 KRNAINIGSNGKFEPLAAKNHITFFYDPTTSBCTSSDVKINNGSAGALNPQGTLLFS 408
DB 357 TRNAIDIASNAKFLNIAATGKNKIFYPDPTTSSG-ATDKLSLNKADGSGNTYEGYVFS 415
QY 409 GETLTADELKVAADLKSSFTQPVSLSGSKLLQGVLTSTSPSOBAGSLMGDSGTTLS 468
DB 416 GKLSSEBELKPKDLKSTFTQAVELAGALVLKQGVTVANNTITQVGSKYVWDGTTFE 475
QY 469 TTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLTIDEGNIYESHMFSDQ 528
DB 476 ASAEVTLNGLAINIDSLDGTNKAILKATPAASKDVALSGPIMLVDAQNYEHHNLISQOQ 535
QY 529 LPSLKITVDADVDNTVNDISLIPVPAEDPNSYEGQGQMNVMWTTDTATNTKATATWT 588
DB 536 VEPPLIELSAQGTW-TTTDLPD--TPILNTNHYGIGQGTIIVWDATAKTAIATLWT 591
QY 589 KTGVPSPERKSAVLCNTLWGVFTDIRSLQOLVEIGATGMEHKQFWSMTNPLKRTGD 648
DB 592 KTGKPNPERQGPLVNSLWGSFVDVRSIQLMDRETSLSSSTNLWVGIAIDFLHEDQK 651
QY 649 ENRKGRHTSGGVITGSAHTPKDDLTFAFCHLPARDQCFIAHNSKRTYGTLEFFKIS 708
DB 652 GNQRSYRHSAGALGAGGFASENFNFAFCQLFQYDQHLVAKNHTVYAGAMSRYR- 710
QY 709 HTLQPNVYLRLGRAKSESAIEKFPREIPLALDVQFSHSDRMETHYTLSPESGSMS 768
DB 711 -----LBSKTLAKILSGNSDSLFPVRNARAYGHIDNNMTTKTGTSPVKGSKG 760
QY 769 NECIAGIGLDPFLVLSNHPLEKTEPIQMKVEMVYVSGNSPFSSSDRGFSGILNLI 828
DB 761 NDAFGIECGGALPVVASGRSWVDHTPLNLEMTIAHQNDFKENGTGGRSFGSEDLFNL 820
QY 829 STVGAKEPQOGDIGDSTYTDLSGFVSDVYRNNPOSTALVMSPDWKIRGNSLQAPL 888
DB 821 AVPVGKIFPK--FSDKSTYDLSTAYVPDVIIRDPCCTTILMVSQDWSYCTGSLRQALL 878
QY 889 LRGSNNVYVNSNCELFHYAMELRGSSRMVNVQVTKLRF 928
DB 879 VRAGNHAFASNFVEFSQFEVLELKGSSRSYALDLDGRPGF 918

RESULT 10
ABP56019
ID ABP56019 standard; protein; 926 AA.

AC ABP56019;
XX
DT 29-AUG-2003 (revised)
DT 25-FEB-2003 (first entry)
XX
XX Chlamydia psittaci antigen CP4#12 protein SEQ ID NO:57.
DE
XX
XX Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
XX Chlamydia; antibacterial; infection.
OS Chlamydia caviae.
XX
XX MO200253588-A2.
XX
XX 11-JUL-2002.
XX
XX 17-DEC-2001; 2001MO-US048715.
XX
XX 15-DEC-2000; 2000US-00738269.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
PI Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B;
XX WPI; 2002-537942/57.
DR N-PSDB; ABQ84775.
XX
PT Vaccine for immunization of animal, preferably bovine, against Chlamydia
PT psittaci, comprises at least one polynucleotide having a C. psittaci
PT sequence, or at least one C. psittaci antigen.
XX
XX Claim 9; Page 158-161; 164pp; English.
XX
CC The present invention describes a vaccine (i) for the immunisation of an
CC animal against Chlamydia psittaci comprising at least one polynucleotide
CC (1a) having a C. psittaci sequence, or at least one C. psittaci antigen
CC (1b), and a carrier. (1a) and (1b) have antibacterial activity. (1) is
CC useful for the immunisation of a bovine. The present sequence represents

CC a C. peltaci antigen from the present invention. (Updated on 29-AUG-2003
 CC to standardise OS field)
 XX
 SO Sequence 926 AA;

Query Match 37.7%; Score 1802; DB 5; Length 926;

Best Local Similarity 40.8%; Pred. No. 4.6e-110;
 Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;

QY 1 MKTSIPWLVSSVLA--FSCHLQSLANBELSPDSEFNGNIDSGTFTPKTSAT---YS 54
 DB 1 MRPELYKILISSTLTLPISFHSQLEHVALTGESIIDAN---GAFSPQSTSTAGGTIYN 57
 QY 55 LTGDFVFEYEPGKGTPLSDSCFKQTTDNLTLFLNGHSLTFEIDAGTAGAAAATTANKL 114
 DB 58 VESDISIVDVQGTAAALASSAFVQJADNLTFRGNHSLISTANAGANPAGINVTADKIL 117
 QY 115 TFSGFSLSFSDSPSTVTYTGQGTLSAGVNLLENIKLVVAGNFSADGAIKGAFL 174
 DB 118 TLTFPSKLSFKECPSSLVNTGKAMKSGALINLANNASILEFDQVYSAENGALISCKAFSL 177
 QY 175 TGTSGDALFSNNSSTKGAIAATTAGARIANNVGFPLSIATSGAIDDEGTSLSN 234
 DB 178 TGSSKEISFTTNTAKKGAIAATGIAHLSDNQGTIFSGNTAVNSGGAIVSEASMTIAG 237
 QY 235 NKFLYFEGNAAKTT---GGAICNTKASGSPDELIISNNKTLIFASNVAETSGAIIHAKL 290
 DB 238 NNHVAFSNNAVSGSDCGAHCSTKGSAPTLTRIDKVLIFRENTISSAKGAIYDKL 297
 QY 291 ALSGCGTFEPLRNWSSATPKGAI SIDAGELSLAETGNTTVRNTLTGSTDTPKR 350
 DB 298 ILTSGGPAPFINNVTATPKGAI GIAANEGCSLLEHGDITR-DNNLMTQDNATIKR 356
 QY 351 NAININGSGKTELEAANKHTIFFFYDPTSECTSDVLKINNGSAGALNPQGTILFSGE 410
 DB 357 NAINIEGKGVNLRPAASGKTIISFYDPTVEGNADLTLLKAGCD--KTYNGAILISGE 414
 QY 411 TLTADELKVDNLKSFSTQPVLSGSKLLLOKGYLTLESTFSQAGSLGMDSGTTLSTT 470
 DB 415 KLTREQAADVADNLKTTFTQPTTLAAGELVLSGVEVEKATVQVAGSILIMDAGTKLSAK 474
 QY 471 AGSITTTMGLINVDSLGKQVSLTAKASMKVIVSGKLANLIDEGNIYESHMSHOLP 530
 DB 475 TEDATLTMLAINPMTLDGKRAVDVAAGKNTLSGAI GVIDPTGKYEHHKINDTLAL 534
 QY 531 SLKITTVDADVDTNVDISLLIPVPAEDPNSXFGQGNVMMTDTATNTEATA--TWT 588
 DB 535 GGIQLSGKGV--TTTNVPSHVGVAE--THYVGQMSVSWVDNNSDPKGTQIAFTWN 590
 QY 589 KTGVPVSPERSALVCNTLWGVFTDIRSLQQLVEIGATG--MEHKQGFVWSMTNPLAKTG 647
 DB 591 KTGVPVNERAPLVNLNLSGSLFIDRSIQVLEKSVDSILETRGLWVSGIGNPFHDKR 650
 QY 648 D-ENRKGRRHNSGCVITGSAHTPKDULTFAPFCHLPARDQCFIAHNNSKTGYTLFEK 706
 DB 651 NAEENK--FRHISGCVYLAATTNTSREDSLSVAFCOLFAKDKQVYLSKNAANVYAGSVYQ 709
 QY 707 HSHLTQPNVYRLGAKFSESAIEKPREIPLADVQVFSHSDRMETHYSLPESEGS 766
 DB 710 HVSXKDDLTRLFNG---PNTCCSFSKEIPIFLDAQTTCYTNANMTTSTTDVPEVGS 765
 QY 767 WSNECIAGIGLDPF-VLSNPHPLFKTFIPQMKVEMYVYVSONSFESSSDGRGFSIGRL 825
 DB 766 WGNDTLGLTLSTVPIVFS--SIFDSVAPFAKLVVYVAHQDDKEPTTEGRVRESSDL 823
 QY 826 LNLSLPVGAKFVQGIIGSYTTLDSGFVSDVYRANPOSTATLWSPSKIRGNLSRQ 885
 DB 824 LNVSVPIGKPEKLSYGERSAYDLTLMYIPVYRHNPSQMTGLAINDVSMILTATNLARQ 883
 QY 886 AFLRGSNNVYVNSCELFGHYAMELRGSSRRYVNDVGTKRF 928
 DB 884 AFTVRAGNHIALTSGVEMPSQGFELRSSSRNRYNDVLGAKVAF 926

RESULT 11

ABB98228 standard; protein; 926 AA.

AC ABB98228;
 XX
 DT 29-AUG-2003 (revised)
 DT 03-OCT-2002 (first entry)
 DE Chlamydia polypeptide SEQ ID NO 57.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

XX Chlamydia; antibacterial; vaccine; immune response; infection.

Dh	238	NNHVAFNNNAVSGSSDDGGGALHCKSTGSAPIITLRDNKVLIFEBEUTSSAKGALITTDKL	297
Qy	291	ALSSGGTFEFLRNNVSSATPKGGAISIDASGELSLSAETGNITFVNNLTITTTGSTDTPKR	350
Dh	298	ILTSGGPAFIANNKTHATPKGGAIGAIANGECSLTAEHGDIIF--DNNIMATODNMTIKR	356
Qy	351	NAINIGSNCKFTELAAKNKHTIFPDPDITSEGTSSVULKINNSAGALNPQOTILPSE	410
Dh	357	NAINIBEGNGFVNLPAAASKTISFPDPIVEGNAADLTILNABGD--KTYNGRIIIFSGR	414
Qy	411	TLTADELKYADVILKSSFTPOVPSLSGGKLLLOKVLTTESTSFSEAGSLGMDGTLSTT	470
Dh	415	KLTEGQAAVADVLLKTTFTPOPIITLAGELVIRSGVEBEATVVOQTAGSLILMDAGTLSAK	474
Qy	471	AGSITITNLGINVDSLGLKQPVSLTAKGASNKIVSGKLNLIIDIEGNIYESHMFSDOLF	530
Dh	475	TEDATLTMLAIHPNLTLDGKKFVAVDAVAAGKVVLTLSGAIQVIDPTEGKFEYENHKLANDTLAL	534
Qy	531	SLUKITIVADVDTNDISLIFVPADPMSSEYGFQGGMMVNNMTTDPATNTKETA--TWT	588
Dh	535	GGIOLSGKSV--TTTNVPSHVGVAB--THYGYQGNMSVSWKDNNSDPKQOTALFTWN	590
Qy	589	KTFEVPSPERKSAIYCNLTLMGVFTDIRSLQOQVEIGATG--MEHKQGFVWSSMNFILHKTG	647
Dh	591	KTGYPNPERRAPVLVNSLMSGFIDLRSLQDVLEKSVBSILETRRLAMVSGICNFPHKR	650
Qy	648	D-ENRKGFRHTSGGYVIGGSAHTPKODLTTFAPCHLFAARDKOCFIAMHNSRTYGTLLPFRK	706
Dh	651	NAENRK--FRHISSSGYVLGATTTISREDSLSVAFCOLFADKDIYVSKNANVYAGSVYQ	709
Qy	707	HSHTLQPNVYLRLGAKPSESALIEKPRRIPLADVQVFSHSNDNMETHYSLSPSEBS	766
Dh	710	HVSKFDDLTRLNPG---PNTCCSGSKSEIPLFLAQITTYCHTANMTTSSYTDYPEVKS	765
Qy	767	WSNECIAAGIGLDLPF-VLSNPHPLFKPTIPOMKEMVNVVSONSPFESSSDRGSGFISRL	825
Dh	766	MGNDTLGLTLSTVSYIIPVSS--SIFDSYAPRAKQYVVAHODDFEAPTEBGEVFESSDL	823
Qy	826	LNLSIPVAKFVQGDIGDSYTYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGGLISRO	885
Dh	824	LNVSPIGIKEFEKLSYGERSAYDLTLMYIPDYVRHNPSCMTGAIINDVSLTTATYMIARQ	883
Qy	886	AFILRGSNMYVNSNCELFGHYAMLELGGSRMYNDVGYKLAFF	928
Dh	884	AFIYPAGNHIALITSGVEMFSGGFELRSSSRMYNDVLAKVAF	926

RESULT 12
ABU66284
ID ABU66284 standard; protein; 926 AA.

AC ABU66284;

DT	23-OCT-2003	(revised)
DT	20-MAY-2003	(first entry)

C. psittaci protein from genomic DNA sequence CP4 #12 #2.

KM Vaccine; chlamydia infection; blindness; mastitis; infertility; abortion;
KM sexually transmitted disease; atherosclerotic plaque;
KM community-acquired pneumonia; coronary heart disease; antigen.

OS Chlamydia caviae.

PN US2002183272-A1.

PD 05-DEC-2002.

PF 17-DEC-2001; 2001US-00023437.

PR 16-AUG-2000; 2000US-0225839P.

XX

PA (JOHN/) JOHNSTON S A.
PA (STEM/) STEMKE-HALE K.
PA (SYKE/) SYKES K F.
PA (KALT/) KALTENBOECK B.
PA

PI Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B, ...

DR WPI; 2003-328634/31.
DR N-PSDB; ABX99200.

PT New vaccine comprising a polynucleotide with a *Chlamydia* sequence or a
PT *Chlamydia* antigen, for inducing an immune response against *Chlamydia*
PT *psittaci*, *Chlamydia pneumoniae*, other *Chlamydia* species, or a non-
PT *Chlamydia* infection.

PS Claim 21; Page 76-78; 100pp; English.

The invention relates to a vaccine comprising a pharmaceutical carrier and at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen. The polynucleotide sequences are obtained from a cloned expression library of fragmented genomic DNA (expressed in the vector pCMV-BD1(+P3). Also included are immunising an animal comprising providing to the animal at least one Chlamydia antigen or its antigenic fragment (expressed from the cloned polynucleotides) to induce an immune response (the proteins are chosen by transforming a vertebrate animal with constituents of the library and choosing those which elicit the best immune response, and then expressing those clones in cell culture and purifying the protein), preparing antibodies against a Chlamydia antigen (comprising identifying a Chlamydia antigen that confers immune resistance against chlamydia bacterial infection when challenged with the Chlamydia species in which the antigen was prepared, generating an immune response in a vertebrate animal with the identified antigen, and obtaining antibodies produced in the animal, the antibodies are used to assay for the presence of chlamydia infection in a vertebrate animal) and testing for antigens for a first disease state/infectious agent (comprising determining an antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide from a second disease state or infectious agent, obtaining a homologue of the antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide from a second disease state or infectious agent for the first disease state/infectious agent, and testing the homology to see if it is an antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide for the first disease state or infectious agent). The vaccine, antigens and polynucleotides are useful for inducing a protective immune response in vertebrate animals against *C. psittaci*, *C. pneumoniae*, other species of Chlamydia, or a non-Chlamydia infection. The antigens are also useful for antibody preparation techniques. Chlamydia species are responsible for blindness, sexually transmitted disease, community-acquired pneumonia and act as co-factors in atherosclerotic plaque formation in coronary heart disease. *C. psittaci* in particular is a cause of mastitis, infertility and abortion in cattle. The present sequence is one of the Chlamydia *psittaci* antigens encoded by a genomic DNA fragment of the invention. (updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 926 AA;

Query Match 37.7%; Score 1802; DB 6; Length 926;

Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;

QY 1 MKTSLPWLVSVA--FSCHLQSLANEELSPDDSFNGNIDSGTFTPKTSATY-----YS 54

Db 1 MRPSLYKILISSTLTPISFHFSQ LHA E VAL TQESILDAN--GAFSPQSTAGGTIYN 57

55 LTGDFVFYEPGKGPLSDSCFKQTNDNLTF LGNGHSLTFGFI DAGTHAGAASTTANKNL 11

Db 58 VESDISIVDVGQTAAALASSAFVQTADNLTFKGNHSLITNANAGANPAGINVTADKIL 11

QY 115 TFGGFSLLSFDSSPSTVTITGGTLSSAGVNLNIRKLVAGNFSTADGAIKGASFL 177

Db 118 TLTFSKLSFKECPSSLVNTGKGAMKSGALNLANNASILFDQNYSAENGGAISCKAFSL 17

QY 175 TGTSGDALFSNNSSSTKGGAIAITAGARIANNTGYVRFLSNIASTSGAIDDEGTSILSN 23


```

Db 178 TGSSKEISFTTNSTAKKGAIATGAIHLSDNQITRFSNGTAVNSGAVYSEASMTIAG 237
Qy 235 NKPLTFEGNAKKT-----GCAICNTKASGSPELLISNNKTLIPASNAETSGAIIHAKKL 290
Db 238 NNHVAFFNNNAVSGSDCGAIHCKSGASPTLTIRNKKVLIPEENTSSAKGAIYVDKL 297
Qy 291 ALSSGCTEFLRNNAVSSATPKGAIISIDAGELSLSAETGNITVRNTLTGTTGSTDTPKR 350
Db 298 ILTSGCTAFLNNKVTATPKGAIIGTANEGCULTHEGDIIT-DNNLWATQONATIKR 356
Qy 351 NAINIGNGKFTELRAAKNHTIFPYDPTSGTSSDVAKINNGSAGALNPYQGTILFSGE 410
Db 357 NAINIEGNGKFTVNRASAGKTISFYDPTVEGNADILTLNKAGD-KTYNGRIIFSGE 414
Qy 411 TLTDDELKVDNKKSSFTQPVLSLGGKLLLOKGYTLESSTPSQAGSLMGDSTLTSTT 470
Db 415 KLTBEQAAVADNKLTTFTPTTLAAGELVLSGVEEAKTVVQFAGSLILMDAGTKLSAK 474
Qy 471 AGSTITNLTGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMSHDOLF 530
Db 475 TEDATLTNLAINPTLDOGKFAVDAVAAGKNTVLSAIGVIDPTGKFEHKKLDLTLAL 534
Qy 531 SLKLTVDADVDTNVDISLLIPEAEDPNSSEYFGQGMVNTTDTATNTKEATA--TWT 588
Db 535 GGIGLGGKGV-TTNNPVSHVGVAE--THYGYQGMVSVGWVNDKNSDPKTOAIPTWN 590
Qy 589 KTGVPSPERKSALVCTMLKVFIDIRSLQOLVETIGATG-MEHQGFVWSMTNPLFKTG 647
Db 591 KTGVPSPERRAPVILNSLWGSFIDLRNIDVLRSDVSIETRRGLWSGIGNPFHKDR 650
Qy 648 D-ENRKGFRRHSGGVVIGSAAHTPKDULFTFAFCHLFARDKDCFIHANNSRTYGTUFPFX 706
Db 651 NAEHRK-FRHSISGVIGLATINTSREBLSVAFCOLFAKDDVLSKNAANVAGSYVYQ 709
Qy 707 HSHLTQPNVYLRGPAKFSESAIEKPREIPLADVOVFSHSDNRMETHYTSLPSEBGS 766
Db 710 HVSFKFDLTRLPNG----PNTCCSGFSKEIRIFILDAQITTYCHTANNMTSTYDPEVYGS 765
Qy 767 WSNECIAGIGLDLPF-VLSNPHLPKFTIFQMVEVMYVYVONSFPRESSGREGFSIGRL 825
Db 766 WGNPTLGLTISTSVPIPVFSS--SIFDSYAPFAKLOVVYAHQDDPKETTEGRVPESSDL 823
Qy 826 LNLISIPVAKFVQCGIDGTYTYDLSGFVSDVYRNNPOSTATLVMSPDMSKIRCGNLSRQ 885
Db 824 LNVSVPIKTEKLSYSGRSAYDLTWMYIPDYRHNPSCMTGLAINDVSMULTATNLARQ 883
Qy 886 AFLLRGSNNVYVNSNCELFGHYAMELRGSSRNVDVGTKLRF 928
Db 884 AFIVRAGNHIALTSGVEMFSGQFGFELRSSRNVDVDAKVAVF 926

```

```

RESULT 13
ABB90542
ID ABB90542 standard; protein; 928 AA.
XX
XX ABB90542;
XX
XX 29-AUG-2003 (revised)
DT 29-JUL-2002 (first entry)
XX
XX Chlamydia pneumoniae cpe731 protein, SEQ ID NO:33.
XX
XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CML029.
XX
XX Chlamydia pneumoniae.
XX
XX Chlamydia pneumoniae.
FH Key Location/Qualifiers
FT Peptide 1..26

```

```

FT /label= Signal_peptide
FT Protein 27..928
FT /note= "Mature protein"
XX
XX WO200202606-A2.
XX
XX 10-JAN-2002.
XX
XX 03-JUL-2001, 2001WO-IB001445.
XX
XX 03-JUL-2000, 2000GB-00016363.
XX
XX 11-JUL-2000, 2000GB-00017047.
XX
XX 21-JUL-2000, 2000GB-00017983.
XX
XX 07-AUG-2000, 2000GB-00019368.
XX
XX 18-AUG-2000, 2000GB-00020440.
XX
XX 14-SEP-2000, 2000GB-00022583.
XX
XX 10-NOV-2000, 2000GB-00027549.
XX
XX 22-DEC-2000, 2000GB-00031706.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Ratti G, Grandi G;
XX
XX WPI, 2002-154726/20.
XX
XX N-PSDB; ABL91200.
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
XX Claim 1; Page 57; 364pp; English.
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
XX pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
XX them. The proteins are predicted to be immunogenic and may therefore be
XX useful in vaccine production and for diagnostic purposes. Chlamydia
XX pneumoniae is a common cause of respiratory disease in humans, and is
XX also involved in the development of cardiovascular diseases such as
XX atherosclerosis, coronary artery disease, carotid artery stenosis,
XX myocardial infarction, cerebrovascular disease, aortic aneurysm,
XX claudication and stroke. The proteins and nucleic acids of the invention
XX may be used in vaccines and pharmaceutical compositions for the
XX prevention or treatment of Chlamydial infections, particularly Chlamydia
XX pneumoniae infections. The proteins may also be used in the detection of
XX Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
XX DNA probe assay or blotting techniques for determining Chlamydia
XX pneumoniae gene expression. The present sequence represents a
XX specifically claimed Chlamydia pneumoniae protein of the invention.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 928 AA:
XX
XX Query Match 37.5%; Score 1794; DB 5; Length 928;
XX Best Local Similarity 42.7%; Pred. No. 1.5e-109; Indels 38; Gaps 17;
XX Matches 404; Conservative 152; Mismatches 353;
XX
XX 1 MKTSIPWLVSSVLAFFSCHLD----SIANEELSPDPSFNGNIDSGTFP-----KTSAT 51
XX 1 MKSILHWFILISSIALPLSLNFGAFAVAVEINLGNPTNSFGC---PGYTPPAQTNADGT 57
XX
XX 52 TYSITGDVFFPEYEPQKGTPLSDSCFKQTTDNLTFLVGNCHSLTFPGFIDAGTHAGAASTTAN 111
XX 58 IYVLTGDSITNAGSPALTPASCFKETTGNIISFGHGVCPLQNIIDAGANIC-TFTYTPAAN 116
XX
XX 112 KNLTFSGFSLSPDSSSTVTYTCQGTLSAGGVNLENIKLVVAGNFSFADGAIKAGS 171
XX 117 KLSLFSFSFYSLSL-IQTNVATGTGAIKSTGACSIQSNVSCYFGQNFSDNGALQGSS 174
XX
XX 172 FLITGTGDALEFNNSSSTGCAIATAGARIANNVTGYVFLSNIASTSGAIDDEGTSI 231
XX 175 ISLS-INPNULTFAKNTKATQKGALYSTGCTITNTLNSASFSENTAANGAIYTEASSF 233
XX
XX 232 LSNKKFLYFEGN--AAKTTGAI-CNTKASGPELLISNNKTLIFASNAETSGAIIHA 287

```

Db	234	ISSNKATISFINNSVTATSATGAIYVCSSTSPAKPVLTLSDNGELNFGNTAITSGAIYLT	293	FT	Region	23.. .31	/label= epitope
Qy	288	KKLALSSGSGTEFLRNK-VSSATPKGAIISIDASGEISLAEFGNTTPVANTLT--TGST	345	FT	Region	53.. .61	/note= "Specifically claimed in claim 12"
Db	294	DNLVSSGGPLTKNNASIDTAAPIADGAIADSGSISLALGGDITFEENTVYKAGSSS	353	FT	Region	57.. .65	/label= epitope
Qy	346	DTEKRNAINIG-SNGKFTLEAAKNHTIFPYDPTSEGS--SDVLKINNGSAGALNPYQ	402	FT	Region	73.. .82	/note= "Specifically claimed in claim 12"
Db	354	QTTTRNSINIGNTNAKIVOLRASGNTTYYPDTTTSITLALSDALNLNGPDLAGNPAYQ	413	FT	Region	73.. .82	/label= epitope
Qy	403	GTLIFSGETLTADLKVADNLIKSPFQVSLSGGKLLLOKVTLESTFSQEAAGSLIGMD	462	FT	Region	90.. .107	/note= "Specifically claimed in claim 12"
Db	414	GTLVFSGEKLEBAADNLKSTIQOPLTLAGQSLKSGVTLLVAKSFQSPGSTLLMD	473	FT	Region	90.. .107	/label= epitope
Qy	463	SGTTLSTTASITITNLGINVDSLGLKQPSLTKAGSNKIVYSGKNLIDIGNTYESH	522	FT	Region	90.. .101	/note= "Specifically claimed in claim 12"
Db	474	AGTTLLETAAD-ITTNLVLVNVDLSIKETKATLAKATQASQVTVLSGLSLVDPGNYVEDV	532	FT	Region	110.. .137	/label= epitope
Qy	523	MFSGHDLFSLKXTVDADVDTNVDISLIPVPAEDPNSSEVFGQGMVNWTTDTATYTK	582	FT	Region	116.. .132	/note= "Specifically claimed in claim 12"
Db	533	SNMNPVFSCLTLT--ADDPANHTITDLADPLEKPIHMGYQGNALSNQEDTATYSKA	590	FT	Region	116.. .132	/label= epitope
Qy	583	ATATWTKTGVPSPERKSALVCTLWGVFTDIBSLQQLVEIGATGMEHKQFVWSMTNF	642	FT	Region	118.. .126	/note= "Specifically claimed in claim 12"
Db	591	ATLTWTKTYGNPBERGTLVANTLWGSFVDVRSIQQLVATKVRQSOETRGIMCEGISNF	650	FT	Region	128.. .136	/note= "Specifically claimed in claim 12"
Qy	643	LHKTGDENRKGFRTSGYITGSAHTPKDULTFAFCHLPADKXCFIAHNSRTYGGT	702	FT	Region	135.. .143	/label= epitope
Db	651	FHKDSTKINKGPFHISAGYVVGATTTTLASDNLITAAFCQLFGKDRDHFINKRASAYAA	710	FT	Region	144.. .160	/note= "Specifically claimed in claim 12"
Qy	703	LFPKHSHTLQPOVYLRGAKFSESATKEPPEIPLADVQVFSHSDNMETHYSLPE	762	FT	Region	144.. .160	/label= epitope
Db	711	LHQLATLTLSSPLRLY--LPGSSS-----EOPVLFDQISITYISKNTMKTYTQAPK	761	FT	Region	159.. .177	/note= "Specifically claimed in claim 12"
Qy	763	SEGSWSNECIAIGIDLPEFVLSPHPLFKTFIPQMKVEMVYVSQNSFFESSD-GRGFS	821	FT	Region	169.. .177	/label= epitope
Db	762	GESSWVNDGALIELASLPHLTALSHBGLFHAAYPPFIIKVEASVYHQDSFKERNITLVRSFD	821	FT	Region	170.. .187	/note= "Specifically claimed in claim 12"
Qy	822	IGLLNLSTIVGAKFVQDIDGDSYTYDLSGFVSDVYRRNPPOSTATLVMSPDMSKIRGN	881	FT	Region	171.. .182	/label= epitope
Db	822	SGDLINVSPIGITFERFSRNERASYEATVYVADVYRKNPDCITJALLINNTSMKTGTN	881	FT	Region	171.. .182	/label= epitope
Qy	882	LSRQAFLLRGSNMYVYVNSCELFGHYAMELRGSSRRNVVGTKLRP	928	FT	Region	178.. .186	/note= "Specifically claimed in claim 12"
Db	882	LSRQAGIGRAGIYFAFSPNLEVTLSMELRGSSRSYNADLGKKPQ	928	FT	Region	195.. .200	/label= epitope
RESULT 14							
ID	ADM65028	ADM65028 standard; protein; 928 AA.					
AC	ADM65028;						
XX	24-MAR-2005	(first entry)					
DE	C. pneumoniae	antigen CP0306.					
XX	Chlamydia pneumoniae	infection; infection; vaccine; antigen;					
KW	antibacterial.						
XX	Chlamydia pneumoniae.						
OS	Key	Location/Qualifiers					
FT	Region	4.. .32					
FT	Region	/label= epitope					
FT	Region	/note= "Specifically claimed in claim 12"					
FT	Region	7.. .16					
FT	Region	/label= epitope					
FT	Region	/note= "Specifically claimed in claim 12"					
FT	Region	8.. .16					
FT	Region	/label= epitope					
FT	Region	/note= "Specifically claimed in claim 12"					
FT	Region	255.. .271					

FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 263. .271
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 277. .287
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 284. .292
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 290. .298
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 291. .314
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 293. .300
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 297. .305
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 310. .318
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 313. .336
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 316. .324
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 324. .332
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 331. .339
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 339. .347
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 344. .350
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 361. .390
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 365. .373
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 369. .375
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 370. .378
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 381. .398
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 383. .391
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 398. .406
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 412. .425
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 413. .421
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 436. .465
FT /label= epitope

FT /note= "Specifically claimed in claim 12"
FT 436. .444
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 443. .451
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 450. .458
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 451. .465
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 454. .462
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 470. .478
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 485. .493
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 487. .496
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 488. .496
FT /label= epitope
FT /note= "Specifically claimed in claim 12"
FT 489. .498
FT /label= epitope
FT /note= "Specifically claimed in claim 12"

Query Match 37.5%; Score 1794; DB 9; Length 928;
Best Local Similarity 42.7%; Pred. No.1.5e-109;
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

Qy 1 MKTSPWLVSVLAASCHQ---SLANEELSPDDSPFNIDSGTFP-----KTSAT 51
Db 1 MKSLHMFLLSSSLALPLSLNPSFAVAWEINLGPNNPSFG---PQTYPPAQTNNADGT 57

Qy 52 TYSLTGDPFPERYERKGPPLSDSCFKOTDRLTFLNGHSLTFPGFIAGTHAAGASTTAN 111
Db 58 TYNLTGDSITTNAGSPALTASCFTKETTGNLSQGHGYOCLONIDAGANC-TFTYTAAN 116

Qy 112 KNLTFSGFSLSPDSSPSTVTVTGOTLSAGGVNENIRKLVVAGNFTADGAIKAS 171
Db 117 KLSFGSFYSL- -IQTNAATTGTGAKSTGACSIQSNVSCYFGQNFSDNGALQGS 174

Qy 172 FLITGTSGDLFENNSSSTGCAIATTAGARINANTGYRFLSNINASTSGAIDDEGTST 231
Db 175 ISLS-LNPNLTFAKNATOKGALYSTGITTINNTLNSASFSENTAANGALYTEASSF 233

Qy 232 LSNKKFLYPEGN--AAKTGGAI-CNTKASGPELIISNNKTLIFASNVAAETSGAIIHA 287
Db 234 ISSNKALSPFNNSVLTATSGAIVCSSTAPRVLTLSDNGELNFTGNATITSGAIIYT 293

Qy 288 KXLALSGCFTEFLRN- -VSSATPKGALSIDASGELS- -SAETGNTTFVNTLT- -TGST 345
Db 294 DNLVLSGCFTLRKNSAIDTAPPLGALIAADSGLSLSALGDITFBEENTVVKASSS 353

Qy 346 DTPKRNAINIG-SNGKTEBLRAKNHTIFPYDITSEGS--SDVLKINNGSGALNIPYQ 402
Db 354 QTTTRNSINIGNTAKIVQLRASQGNITVFYDITTSITTAALDANLNPDLAGPAYQ 413

Qy 403 GTILFSGETLTADBLKXADNLKSFQPVLSGSKLLQGVTLSESTFSGQAGSLIGMD 462
Db 414 GTIVFSGEKSEBAADNLKSTIQPFLTAGQSLSGSVTLVASFSQSGOSTLMD 473

Qy 463 SGTTLSTAGSITITNGLINVDLSGLKQPVSLTAKGASNKVIYSGKLNLIIDIGNIYESH 522
Db 474 AGTTLERADG-ITINNVLAVNDLSIKETKATLAKATQASQVVTLSGSLSLVDPSGVYEDV 532
Qy 523 MFSHQQLFSLKITTVDADVDVTNVDISSLIPVPAEDPNSERYFGQGMNVNMTTDTATNKE 582

```

Db      533 SWNNPQVFSCLTTLT--ADDPANIHITDLADPLEKNIHWGOGNNWALSMQEDTATKSKA 590
      583 ATATWTKTGVPSPERSKALVNTLWGVFPIRDISLOOLVIGATGMHKGQFVWSSMTNF 642
      591 ATLTWTKTGNPNERRGTLVANTLWGSFVDVRSIQOLVATKVRQSGETGICEGISNF 650
Qy      643 LHKTDENRKGFRHTSGGYVIGGSAHPKDDLTFFAPCHLPARDKCFIAHNNSTRYGGT 702
      651 FHHDSRTKINGKGFHISAGYVVGATTTLASDNLITAAFCQLFGDRDRHFINKNAAVAAS 710
Qy      703 LFFKHSHTLOPQNYLRLGRAKFSBSAIEKFPREIPLALDVQVSESHSDNMEHTYSLPE 762
      711 LHKQHLATLSSPLLRY--LPGSBS-----EQPVLPDAQISYISKNTMKTYTQAPK 761
Qy      763 SEGSWSNECIAGIGLDLPFVLSNPHLPFKTFIPOMVENVVYVYVSSQNSFFESSSD-GRGFS 821
      762 GESSWYNDGCALBLASSLPHTALSHBGLFHAHYFPFKIVEASYIHQDSFKERNITLVRSFD 821
Qy      822 IGRLLNLISIPVGAKEFVQGDIGDSTYTDLSGFVSDVYVRNNPOSTATLWVSPDWKIRGCN 881
      822 SGDLINVSPIGITFERFSRNERASYEATYIVADYVRKRPDCTTALLINNTSMKTGTGN 881
Db      882 LSRQALRLGSNNYVNSNCELFGHYAMELRGSSRNYNVDVGTKLRF 928
      882 LSRQAGIGRAGIFYAFSPNLEVTSNLSMEIRGSSRSYNADLGKQFQF 928

```

RESULT 15
AAW88423
ID AAW88423 standard; protein; 928 AA.

XX AAW88423;

XX 17-OCT-2003 (revised)
XX 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp10.

XX Omp10; outer membrane protein 10; surface exposed protein; antigen;
XX infection; diagnosis; vaccine; atherosclerosis; asthma.

XX Chlamydophilia pneumoniae.

XX W09858953-A2.

XX 30-DEC-1998.

XX 19-JUN-1998; 98MO-DK000266.

XX 23-JUN-1997; 97DK-00000744.

XX (BIRK/) BIRKELUND S.
XX (CHRI/) CHRISTIANSEN G.

PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

XX WPI; 1999-105610/09.

XX N-PSDB; AAX06822.

XX Species-specific test for identifying mammals infected with Chlamydia
XX pneumoniae - comprises detecting antibodies specific for outer membrane
XX proteins of C. pneumoniae or nucleic acids encoding these proteins.

XX Claim 7, Page 60-62; 115pp; English.

XX This polypeptide comprises the novel 98.4 kDa surface exposed protein
XX Omp10 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
XX acid sequence was deduced from DNA (see AAX06822) isolated from a C.
XX pneumoniae expression library. The invention provides 12 novel surface
XX exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid
XX sequences encoding them (see AAX06816-27). A new species specific test is
XX claimed that is used to identify mammals (including humans) infected with

CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
CC proteins can also be used in the immunization of mammals, the nucleic
CC acids being particularly useful as DNA vaccines for effecting in vivo
CC expression of antigens. The vaccines may also prevent atherosclerosis and
CC bronchial asthma, which are possibly associated with C. pneumoniae.
CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 928 AA;

Query Match 37.5%; Score 1793; DB 2; Length 928;
Best Local Similarity 42.6%; Pred. No. 1.8e-109;
Matches 403; Conservative 153; Mismatches 353; Indels 38; Gaps 17;

```

Qy      1 MKTSIRWVVSSTLAFASCHIQ-----SLANBELSPDSSNGNIDSGTTP-----KTSAT 51
      1 MKSILMFVYISSSLAPLSLNSAFAAVEINLGPNSFSG--PQTYTPPAQTNNADGT 57
Db      52 TYSLTGDPFVEYERKGTPLSDSCFKOTTDNLTFLGNHSLTFGFDAGTHAGAASTTAN 111
      58 IYNLTGDPVSTINAGSTALTAFCFKETGNLSFGHGYPFLONIDAGANC-ITFTTAA 116
Qy      112 KULTFESGFSLSPDSSPTVTGQTLSSAGGVNLENIKLVVAGNFTADGAIKAS 171
      117 KILSFGSFGYSLD--IQTNATGTGAIKSTGACSIQSNVSCYFGQNFSDNMGALOGSS 174
Qy      172 FLITGTSGLALPSNNSSTKGGALATTAGARLANNTGYRFLSNIASTSGAALDDEGT 211
      175 ISLS-LNPNLTPAKNATQKGALYSTGITTINNTLNSASFEBNTAANNAGALYTTASSP 233
Qy      232 LSNKFLYPEGN---AAKTGGAI-CNTKASGPELIISNNKTLIPASVVAETSGAIIHA 287
      234 ISNNKAISFTNNSVYATSAITGAIYCSSTSAKPPVLTLDNGELNITGNTAITSGAIIY 293
Qy      288 KKLALSSGPFTEPLRNN-VSATPKGAISIDAGSLSAETGNITFVRNTLTT-TGST 345
      294 DNLVSSGGPTLPKNNSAIDTAPLGAIAIDSGSLSLALGGDITFGNTVVKACASS 353
Qy      346 DTPKRAINIG-SNGFTELPAAKNTTFYDPITSEGS--SDVUKINNGAGALNPQ 402
      354 QTTNRNSINIGNTAKIVQLRASQGNITFYDPITTNHAAISDALNLPDLAAGPAVQ 413
Qy      403 GTILFSGENTLTDELKVADNLKSSFTQPVLSGGKLLQGVTLFESTSQAEGSLIGMD 462
      414 GTIVSGEKLSKAEADNLKSTIQPLTLAGGQLSLSGVTLVAKSSQSGSLTMD 473
Qy      463 SGTTLSTTAGSITITNIGINVDSLGKQPVSLTAKASNKVIYVSGKLNLDIBGNIESH 522
      474 AGTTLETADG-ITINNVLNVDSIKETKATLKATQASQTVTLJSGLSLYDPEGNYEDV 532
Qy      523 MESHDLFSLKLTVDADVDVNDVSSLIIPVPAEDNSEYGGOGNNVAMTTDTANTYKE 582
      533 SWNNPQVFSCLTTLT--ADDPANIHITDLADPLEKNIHWGOGNNWALSMQEDTATKSKA 590
Qy      583 ATATWTKTGVPSPERSKALVNTLWGVFPIRDISLOOLVIGATGMHKGQFVWSSMTNF 642
      591 ATLTWTKTGNPNERRGTLVANTLWGSFVDVRSIQOLVATKVRQSGETGICEGISNF 650
Qy      643 LHKTDENRKGFRHTSGGYVIGGSAHPKDDLTFFAPCHLPARDKCFIAHNNSTRYGGT 702
      651 FHHDSRTKINGKGFHISAGYVVGATTTLASDNLITAAFCQLFGDRDRHFINKNAAVAAS 710
Qy      703 LFFKHSHTLOPQNYLRLGRAKFSBSAIEKFPREIPLALDVQVSESHSDNMEHTYSLPE 762
      711 LHKQHLATLSSPLLRY--LPGSBS-----EQPVLPDAQISYISKNTMKTYTQAPK 761
Qy      763 SEGSWSNECIAGIGLDLPFVLSNPHLPFKTFIPOMVENVVYVYVSSQNSFFESSSD-GRGFS 821
      762 GESSWYNDGCALBLASSLPHTALSHBGLFHAHYFPFKIVEASYIHQDSFKERNITLVRSFD 821
Qy      822 IGRLLNLISIPVGAKEFVQGDIGDSTYTDLSGFVSDVYVRNNPOSTATLWVSPDWKIRGCN 881

```

Mon Nov 28 09:39:53 2005

us-09-446-677b-2.rag

Page 16

Db 822 SGDLINVSVIGTIFERFSRNEFASIEATVIVYADYRKNPDCITALLINNTSKTTGTN 881

Qy 882 LSRQAFLLRGSNMYVYNSNCELFCHAMELRGSSRRNVYDGTKLRF 928

Db 882 LSRQAGIGRAGIIFYAFSPNLEVTNSNLSMEIRRSSSYNADLGKQKF 928

Search completed: November 25, 2005, 14:10:21
Job time : 113.98 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:02:05 / Search time 24.1039 Seconds
(without alignments)
3704.345 Million cell updates/sec

Title: US-09-446-677B-2

Sequence: 1 MKTSIPWLVSSVLAFLPSCHL.....MELRGSSRNVDVGTGLRF 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4782	100.0	928	2	D72077 polymorphic outer
2	4782	100.0	928	2	H86546 polymorphic outer
3	4782	100.0	949	2	F81591 polymorphic membra
4	1794	37.5	928	2	B72077 polymorphic membra
5	1794	37.5	928	2	B86546 polymorphic outer
6	1785	37.3	928	2	G86546 polymorphic outer
7	1785	37.3	928	2	G81591 polymorphic membra
8	1763	36.9	930	2	D86546 polymorphic outer
9	1763	36.9	930	2	A81591 polymorphic membra
10	1761	36.8	930	2	D72078 polymorphic outer
11	1734	36.3	936	2	C72078 polymorphic outer
12	1733	36.2	936	2	B81591 polymorphic membra
13	1733	36.2	936	2	C86546 polymorphic outer
14	1591	33.3	772	2	H86492 Pmp_3 [imported] -
15	1435.5	30.0	841	2	E72130 polymorphic membra
16	1353	28.3	922	2	B72131 polymorphic outer
17	1353	28.3	922	2	B86491 polymorphic outer
18	1352	28.3	922	2	F81539 polymorphic membra
19	1284.5	26.9	973	2	B86547 polymorphic outer
20	1284.5	26.9	973	2	F72076 polymorphic outer
21	1284.5	26.9	995	2	C81593 polymorphic membra
22	1203	25.2	1276	2	B86546 polymorphic outer
23	1203	25.2	1276	2	C81591 polymorphic membra
24	1164	24.3	712	2	E86492 polymorphic outer
25	1144.5	23.9	1407	2	B72078 polymorphic outer
26	1102.5	23.1	1013	2	G71460 probable outer mem
27	1040	21.7	987	2	H81722 polymorphic membra
28	843.5	17.6	494	2	D86493 polymorphic outer
29	837	17.5	878	2	B71460 probable outer mem

30	831.5	17.4	427	2	A86493 polymorphic outer
31	829.5	17.3	867	2	F81721 polymorphic membra
32	790	16.5	445	2	E86493 Pmp_5 [imported] -
33	736.5	15.4	359	2	C86493 Pmp_4 [imported] -
34	679.5	14.2	947	2	D72067 polymorphic membra
35	678.5	14.2	947	2	G86557 polymorphic membra
36	610.5	12.8	964	2	E71460 probable outer mem
37	610.5	12.8	1723	2	H86557 polymorphic membra
38	610.5	12.8	1723	2	E72067 polymorphic membra
39	610.5	12.8	1732	2	C81601 polymorphic membra
40	608.5	12.7	978	2	C86547 polymorphic outer
41	608.5	12.7	978	2	B81593 polymorphic membra
42	604.5	12.6	986	2	B81675 polymorphic membra
43	604	12.6	1016	2	H71460 probable outer mem
44	603.5	12.6	978	2	G72076 polymorphic outer
45	600.5	12.6	934	2	G86548 polymorphic outer

ALIGNMENTS

RESULT 1

D72077 polymorphic outer membrane protein g family - Chlamydia pneumoniae (strain CWL029)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: D72077

R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A/Reference number: A72000; MUID:99206606; PMID:10192388

A/Accession: D72077

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-928 <ARN>

A/Cross-references: UNIPROT:O86164; UNIPARC:UPI000002FFEF; GB:AE001628; GB:AE001363; NID:

A/Experimental source: strain CWL029

C/Genetics:

A/Gene: pmp_11

C/superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match	100.0%	Score 4782	DB 2	Length 928
Best Local Similarity	100.0%	Pred. No. 1.5e-261		
Matches	928	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	1	MKTSIPWLVSSVLAFLPSCHLQSLANEELSPDSEFGNIDSGTFPKTSATYSLGDFV	60	
DB	1	MKTSIPWLVSSVLAFLPSCHLQSLANEELSPDSEFGNIDSGTFPKTSATYSLGDFV	60	
QY	61	FYEPKGTPLDSPSCFQKQTDNLTFLNGHSLTFGFIDAGTHAGAAATYANKRLTFESGS	120	
DB	61	FYEPKGTPLDSPSCFQKQTDNLTFLNGHSLTFGFIDAGTHAGAAATYANKRLTFESGS	120	
QY	121	LISFDSPTTYTGGGLTSSAGVNLRIKLVAAGNFSTADGAIKCAFLTGTSGD	180	
DB	121	LISFDSPTTYTGGGLTSSAGVNLRIKLVAAGNFSTADGAIKCAFLTGTSGD	180	
QY	181	ALFSNNSSSTKGALATTGARIANTGYVRLSNASTSGAIDDEGSIIISNNFLVF	240	
DB	181	ALFSNNSSSTKGALATTGARIANTGYVRLSNASTSGAIDDEGSIIISNNFLVF	240	
QY	241	EGNAAKTTGCAICNTKASGPELIISNNKTLIFASVNAETSGAIIHAKKLALSSGFTFF	300	
DB	241	EGNAAKTTGCAICNTKASGPELIISNNKTLIFASVNAETSGAIIHAKKLALSSGFTFF	300	
QY	301	LNNVSSATPKGGAISIDASGELSASFTGNTTFVAVNTLTGGSTDTPPKRNAINISNGK	360	
DB	301	LNNVSSATPKGGAISIDASGELSASFTGNTTFVAVNTLTGGSTDTPPKRNAINISNGK	360	
QY	361	FEELRAKNTTFFPDITSEGTSSDVLLKINNAGALNPYGTILFSGETTLTADLKYA	420	
DB	361	FEELRAKNTTFFPDITSEGTSSDVLLKINNAGALNPYGTILFSGETTLTADLKYA	420	

QY 421 DNKSSFTQPVSLGGKLLQKGVLTLESTSPSOAGSLGMDSGTLLTAGSITTTNLG 480
DB 421 DNKSSFTQPVSLGGKLLQKGVLTLESTSPSOAGSLGMDSGTLLTAGSITTTNLG 480
QY 481 INVDLSGLKQPVSLTAKGASNKVIYVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
DB 481 INVDLSGLKQPVSLTAKGASNKVIYVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
QY 541 VDTNVDLSSLLPVAEDPNSIEYFQOGQNNVMTTDTAINTKEATATWTGTGFPVSPERKS 600
DB 541 VDTNVDLSSLLPVAEDPNSIEYFQOGQNNVMTTDTAINTKEATATWTGTGFPVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNLFHKTGDENRKGFRTSSGG 660
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNLFHKTGDENRKGFRTSSGG 660
QY 661 YVIGGSATHTPKDDLFTFAFCHLFPARDKCFIAHNNSTRYGGTLFPFKSHITLQPNYLRLG 720
DB 661 YVIGGSATHTPKDDLFTFAFCHLFPARDKCFIAHNNSTRYGGTLFPFKSHITLQPNYLRLG 720
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHYTSLPESGSMNECTIAGIGLGL 780
DB 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHYTSLPESGSMNECTIAGIGLGL 780
QY 781 PFVLSNPHPLFKFTIPQMKVEMVYVSONSPFESSSDRGFSIGRLNLSIPVGAKEVQGD 840
DB 781 PFVLSNPHPLFKFTIPQMKVEMVYVSONSPFESSSDRGFSIGRLNLSIPVGAKEVQGD 840
QY 841 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGGLSRQAFLLRGSNNYVNSN 900
DB 841 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGGLSRQAFLLRGSNNYVNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 2
H86546
polymorphic outer membrane protein G family [imported] - Chlamydia pneumoniae (strain
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86546
R:Shirai, M.; Hixkawa, H.; Kimoto, M.; Tabuchi, M.; Kishii, F.; Ouchi, K.; Shiba, T.; Ii
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; PMID:20330349; PMID:10871362
A:Accession: H86546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <STO>
A:Cross-references: UNIPROT:086164; UNIPARC:UPI000002PFEBF; GB:BA000008; NID:g8978822; PI
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_11
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 4782; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 1.5e-261;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSLPWLIVSVSLAFSCHLOSLANEELLSPDPSFNGNIDSGTFTPKTSATTVSLTGDF 60
DB 1 MKTSLPWLIVSVSLAFSCHLOSLANEELLSPDPSFNGNIDSGTFTPKTSATTVSLTGDF 60
QY 61 FYEPEKGPLDSCFKQTTDNITFLGNGHSLTFGIDAGTAGAASATTANKNLTFSGFS 120
DB 61 FYEPEKGPLDSCFKQTTDNITFLGNGHSLTFGIDAGTAGAASATTANKNLTFSGFS 120
QY 121 LLSFSSSTTYTTCOGTLLSAGVNLNIRKLVVAGNPSADGAGIIGASFTLGTSGD 180
DB 121 LLSFSSSTTYTTCOGTLLSAGVNLNIRKLVVAGNPSADGAGIIGASFTLGTSGD 180

QY 181 ALFSNNSSSTKGALATTAGARIANNNTGYRFLSNIASTSGAIDDEGTSILSNKKFLYF 240
DB 181 ALFSNNSSSTKGALATTAGARIANNNTGYRFLSNIASTSGAIDDEGTSILSNKKFLYF 240
QY 241 EGNAAATGGALICNTASGSPELLISNNKTLFASVVAETSGGAIHAKKLLASSGGFTTF 300
DB 241 EGNAAATGGALICNTASGSPELLISNNKTLFASVVAETSGGAIHAKKLLASSGGFTTF 300
QY 301 LRNNVSAATPKGALSIDASGELSIAETGNITFVANTLTGTSDDTPKRNAINISNGK 360
DB 301 LRNNVSAATPKGALSIDASGELSIAETGNITFVANTLTGTSDDTPKRNAINISNGK 360
QY 361 FTFLRAKNTHTFFYPDITSEGTSDVLKINNSAGALNPQGTILFSGETLTADBLKTA 420
DB 361 FTFLRAKNTHTFFYPDITSEGTSDVLKINNSAGALNPQGTILFSGETLTADBLKTA 420
QY 421 DNKSSFTQPVSLGGKLLQKGVLTLESTSPSOAGSLGMDSGTLLTAGSITTTNLG 480
DB 421 DNKSSFTQPVSLGGKLLQKGVLTLESTSPSOAGSLGMDSGTLLTAGSITTTNLG 480
QY 481 INVDLSGLKQPVSLTAKGASNKVIYVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
DB 481 INVDLSGLKQPVSLTAKGASNKVIYVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
QY 541 VDTNVDLSSLLPVAEDPNSIEYFQOGQNNVMTTDTAINTKEATATWTGTGFPVSPERKS 600
DB 541 VDTNVDLSSLLPVAEDPNSIEYFQOGQNNVMTTDTAINTKEATATWTGTGFPVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNLFHKTGDENRKGFRTSSGG 660
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNLFHKTGDENRKGFRTSSGG 660
QY 661 YVIGGSATHTPKDDLFTFAFCHLFPARDKCFIAHNNSTRYGGTLFPFKSHITLQPNYLRLG 720
DB 661 YVIGGSATHTPKDDLFTFAFCHLFPARDKCFIAHNNSTRYGGTLFPFKSHITLQPNYLRLG 720
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHYTSLPESGSMNECTIAGIGLGL 780
DB 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHYTSLPESGSMNECTIAGIGLGL 780
QY 781 PFVLSNPHPLFKFTIPQMKVEMVYVSONSPFESSSDRGFSIGRLNLSIPVGAKEVQGD 840
DB 781 PFVLSNPHPLFKFTIPQMKVEMVYVSONSPFESSSDRGFSIGRLNLSIPVGAKEVQGD 840
QY 841 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGGLSRQAFLLRGSNNYVNSN 900
DB 841 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGGLSRQAFLLRGSNNYVNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 3
F81591
polymorphic membrane protein G family CP0302 [imported] - Chlamydia pneumoniae (strain
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C:Accession: F81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heldelberg, J.F.; White, O.; Hickey, J.
, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Moyn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; PMID:20150255; PMID:10684935
A:Accession: F81591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-949 <REA>
A:Cross-references: UNIPARC:UPI00001655FA; GB:AE002192; GB:AE002161; NID:97189226; PIDN:J
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0302
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 4782; DB 2; Length 949;
Best Local Similarity 100.0%; Pred. No. 1.5e-261;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSPVWLVSVLAFCCHLOSLANBELSPDPSFNGNIDSGTPTKTSATYSLTGDFV 60
DB MKTSPVWLVSVLAFCCHLOSLANBELSPDPSFNGNIDSGTPTKTSATYSLTGDFV 81
QY FYEKGKTPISDSGCFKOTDNLFTLGNGHSLTFEFTAGTAGAGAAATANKLTFSGFS 120
DB FYEKGKTPISDSGCFKOTDNLFTLGNGHSLTFEFTAGTAGAGAAATANKLTFSGFS 141
QY LLSFSSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGSFLLTGSGD 180
DB LLSFSSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGSFLLTGSGD 201
QY LLSFSSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGSFLLTGSGD 201
DB LLSFSSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGSFLLTGSGD 201
QY ALFSSNNSSTKGAIATTAGARIANNTGYVFLSNIASTSGAIDEGTSLSNKFLYF 240
DB ALFSSNNSSTKGAIATTAGARIANNTGYVFLSNIASTSGAIDEGTSLSNKFLYF 261
QY EGNAAKTGGAICTTKASGSEPELLIINNKTILFASNAETSGAIIHAKKLLASGSETER 300
DB EGNAAKTGGAICTTKASGSEPELLIINNKTILFASNAETSGAIIHAKKLLASGSETER 321
QY LKNNVSSATPKGAIISIDASGELSASATGNITFVRWTLTTTGSTDPKRNAINIGSNGK 360
DB LKNNVSSATPKGAIISIDASGELSASATGNITFVRWTLTTTGSTDPKRNAINIGSNGK 381
QY LKNNVSSATPKGAIISIDASGELSASATGNITFVRWTLTTTGSTDPKRNAINIGSNGK 381
DB LKNNVSSATPKGAIISIDASGELSASATGNITFVRWTLTTTGSTDPKRNAINIGSNGK 381
QY FTELRAKKNHTIFPYDPITSEGTSSDYKINNGSAGALNPQGTILFSGETLTADELKVA 420
DB FTELRAKKNHTIFPYDPITSEGTSSDYKINNGSAGALNPQGTILFSGETLTADELKVA 441
QY DNKSSFTQPSVLSGGKLLQKGTLESTSPQASGLLMDSTLTSTAGSTTTNIG 480
DB DNKSSFTQPSVLSGGKLLQKGTLESTSPQASGLLMDSTLTSTAGSTTTNIG 501
QY DNKSSFTQPSVLSGGKLLQKGTLESTSPQASGLLMDSTLTSTAGSTTTNIG 501
DB DNKSSFTQPSVLSGGKLLQKGTLESTSPQASGLLMDSTLTSTAGSTTTNIG 501
QY INVDSLQKQVSLTAKGASNKVIVSGKLLIDIEGNIYESHMSHQLFSLKITVDAD 540
DB INVDSLQKQVSLTAKGASNKVIVSGKLLIDIEGNIYESHMSHQLFSLKITVDAD 561
QY INVDSLQKQVSLTAKGASNKVIVSGKLLIDIEGNIYESHMSHQLFSLKITVDAD 561
DB INVDSLQKQVSLTAKGASNKVIVSGKLLIDIEGNIYESHMSHQLFSLKITVDAD 561
QY VDTNVDISSLI PVAEDPNSBYFGQGMVNMVTTDTATNTKEATATVTKGFVSPERKS 600
DB VDTNVDISSLI PVAEDPNSBYFGQGMVNMVTTDTATNTKEATATVTKGFVSPERKS 621
QY VDTNVDISSLI PVAEDPNSBYFGQGMVNMVTTDTATNTKEATATVTKGFVSPERKS 621
DB VDTNVDISSLI PVAEDPNSBYFGQGMVNMVTTDTATNTKEATATVTKGFVSPERKS 621
QY ALVNTLMGVPTDTRSLQOLVEIGATGMEHKQGFVWSMTNFKLKTGDENRKGRHTSG 660
DB ALVNTLMGVPTDTRSLQOLVEIGATGMEHKQGFVWSMTNFKLKTGDENRKGRHTSG 681
QY ALVNTLMGVPTDTRSLQOLVEIGATGMEHKQGFVWSMTNFKLKTGDENRKGRHTSG 681
DB ALVNTLMGVPTDTRSLQOLVEIGATGMEHKQGFVWSMTNFKLKTGDENRKGRHTSG 681
QY YVIGGSATPDDLFPAFCHLFAFDKOCFIAHNSRTYGGTLFPGKSHTLQPNYRLIG 720
DB YVIGGSATPDDLFPAFCHLFAFDKOCFIAHNSRTYGGTLFPGKSHTLQPNYRLIG 741
QY YVIGGSATPDDLFPAFCHLFAFDKOCFIAHNSRTYGGTLFPGKSHTLQPNYRLIG 741
DB YVIGGSATPDDLFPAFCHLFAFDKOCFIAHNSRTYGGTLFPGKSHTLQPNYRLIG 741
QY RAKESGAIEKFPREIPLADVOVFSHSDNRMETHTSLPESGSMNEICAGIGLDL 780
DB RAKESGAIEKFPREIPLADVOVFSHSDNRMETHTSLPESGSMNEICAGIGLDL 801
QY RAKESGAIEKFPREIPLADVOVFSHSDNRMETHTSLPESGSMNEICAGIGLDL 801
DB RAKESGAIEKFPREIPLADVOVFSHSDNRMETHTSLPESGSMNEICAGIGLDL 801
QY PFLVLSNHPLEKTIIPQKYMVMYVSONSPFESSDGRGFSIGLMLSLIPVAKKFOGD 840
DB PFLVLSNHPLEKTIIPQKYMVMYVSONSPFESSDGRGFSIGLMLSLIPVAKKFOGD 861
QY PFLVLSNHPLEKTIIPQKYMVMYVSONSPFESSDGRGFSIGLMLSLIPVAKKFOGD 861
DB PFLVLSNHPLEKTIIPQKYMVMYVSONSPFESSDGRGFSIGLMLSLIPVAKKFOGD 861
QY IGDSYTVDSLGSFVSDYVRNNPOSTATLWMSPDWKIRGNLISOAFLNGSNNYVNSN 900
DB IGDSYTVDSLGSFVSDYVRNNPOSTATLWMSPDWKIRGNLISOAFLNGSNNYVNSN 921
QY IGDSYTVDSLGSFVSDYVRNNPOSTATLWMSPDWKIRGNLISOAFLNGSNNYVNSN 921
DB IGDSYTVDSLGSFVSDYVRNNPOSTATLWMSPDWKIRGNLISOAFLNGSNNYVNSN 921
QY CELFGHYAMELRGSSRYNVVDVGTCLRF 928
DB CELFGHYAMELRGSSRYNVVDVGTCLRF 949

RESULT 4
B72077
polymorphic membrane protein G family CP0306 [imported] - Chlamydomphila pneumoniae (str)

C:Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_reviseion 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: B72077; B81592
R:Kallman, S.; Mitchell, W.; Marache, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; PMID:99206606; PMID:10192388
A:Accession: B72077
A:Molecule type: DNA
A:Residues: 1-928 <ARN>

A:Cross-references: UNIPROT:Q9Z388; UNIPARC:UPI0000047087; GB:AE001628; GB:AE001363; NID:
A:Experimental source: strain CML029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; PMID:20150255; PMID:10684935
A:Accession: B81592
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: UNIPARC:UPI0000047087; GB:AE002192; GB:AE002161; NID:97189226; PIDN:
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: pmp_9; CP0306
C:Superfamily: Chlamydomphila pneumoniae polymorphic outer membrane protein G

Query Match 37.5%; Score 1794; DB 2; Length 928;
Best Local Similarity 42.7%; Pred. No. 3e-93;
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

QY 1 MKTSPVWLVSVLAFCCHLOSLANBELSPDPSFNGNIDSGTPTKTSATYSLTGDFV 51
DB 1 MKTSPVWLVSVLAFCCHLOSLANBELSPDPSFNGNIDSGTPTKTSATYSLTGDFV 57
QY TYSLTGDFVFPYEPKGTPLSDSCFKOTDNLFTLGNGHSLTFEFTAGTAGAGAAATANK 111
DB TYSLTGDFVFPYEPKGTPLSDSCFKOTDNLFTLGNGHSLTFEFTAGTAGAGAAATANK 116
QY 112 KNTFSGFSLSFSDSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGS 171
DB 112 KNTFSGFSLSFSDSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGS 174
QY 117 KNTFSGFSLSFSDSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGS 174
DB 117 KNTFSGFSLSFSDSPSTVTYTGQGTLSAGGVNLENIRKLVVAGNFSTADGAIKGS 174
QY 172 FLTGSGDALPSSNNSSTKGAIATTAGARIANNTGYVFLSNIASTSGAIDEGTSL 231
DB 172 FLTGSGDALPSSNNSSTKGAIATTAGARIANNTGYVFLSNIASTSGAIDEGTSL 233
QY 175 ISLS-LNPULTFAKKNATQKGAIVSTGTTINTLNSASFSTANNGAIYTEASSF 233
DB 175 ISLS-LNPULTFAKKNATQKGAIVSTGTTINTLNSASFSTANNGAIYTEASSF 233
QY 232 LSNKFLYEBGN--AAKTGGAI-CTTKASGSEPELLIINNKTILFASNAETSGAIIH 287
DB 232 LSNKFLYEBGN--AAKTGGAI-CTTKASGSEPELLIINNKTILFASNAETSGAIIH 293
QY 234 ISSNKAISFINNSVATSAATGAIYCSSTAPKPVTLSDNGELNFIGMTAITSAGAIY 293
DB 234 ISSNKAISFINNSVATSAATGAIYCSSTAPKPVTLSDNGELNFIGMTAITSAGAIY 293
QY 288 KKLASSGSETEFLRNK-VSSATPKGAIISIDASGELSASATGNITFVRNLTIT--TGS 345
DB 288 KKLASSGSETEFLRNK-VSSATPKGAIISIDASGELSASATGNITFVRNLTIT--TGS 353
QY 294 DNLVSSGGPTLFPKNSAIDTAPALGAIADDSGLSLSAGGDTTFEGNTVVKASSS 353
DB 294 DNLVSSGGPTLFPKNSAIDTAPALGAIADDSGLSLSAGGDTTFEGNTVVKASSS 353
QY 346 DTPKRNAINIG-SNGKFTLRAKKNHTIFPYDPITSEGTSSDYKINNGSAGALNPYQ 402
DB 346 DTPKRNAINIG-SNGKFTLRAKKNHTIFPYDPITSEGTSSDYKINNGSAGALNPYQ 413
QY 354 QTTTRNSINIGNNAIYQLRASQNTIIFYDPITSTIRALSDALNNGPDLAAGPAVQ 413
DB 354 QTTTRNSINIGNNAIYQLRASQNTIIFYDPITSTIRALSDALNNGPDLAAGPAVQ 413
QY 403 GTLFSGETLTADELKVAENLKSFTQPSVLSGGKLLQKGTLESTSPQASGLLMD 462
DB 403 GTLFSGETLTADELKVAENLKSFTQPSVLSGGKLLQKGTLESTSPQASGLLMD 473
QY 414 GTLVFSGEKLSEAEADNLKSTIQPPLTAGGQSLKSGVTLVAKSFGSGSTLMD 473
DB 414 GTLVFSGEKLSEAEADNLKSTIQPPLTAGGQSLKSGVTLVAKSFGSGSTLMD 473
QY 463 SCFTLSTAGSTTTTTLGNNDSLGKQVSLTAKGASNKVIVSGKLLIDIEGNIYESH 522
DB 463 SCFTLSTAGSTTTTTLGNNDSLGKQVSLTAKGASNKVIVSGKLLIDIEGNIYESH 532
QY 474 AGTTLTAAG-ITINNVLNVDLSKETKATLAKVQASQVTLVSSGLSLVDSGANVYEV 532
DB 474 AGTTLTAAG-ITINNVLNVDLSKETKATLAKVQASQVTLVSSGLSLVDSGANVYEV 532
QY 523 MESHDLFSLKITVDADVTNVDISSLI PVAEDPNSBYFGQGMVNMVTTDTATNTKE 582
DB 523 MESHDLFSLKITVDADVTNVDISSLI PVAEDPNSBYFGQGMVNMVTTDTATNTKE 590
QY 533 SMNVPQVFCITLT--ADDPANIHITDLADAPLEKXPHIMVGQGNALMAGBETAKSKA 590
DB 533 SMNVPQVFCITLT--ADDPANIHITDLADAPLEKXPHIMVGQGNALMAGBETAKSKA 590
QY 583 ATATWTKTGVPSPERKALVCNTLWGVFTDTRSLQOLVEIGATGMEHKQGFVWSMTN 642
DB 583 ATATWTKTGVPSPERKALVCNTLWGVFTDTRSLQOLVEIGATGMEHKQGFVWSMTN 650

Qy	643	LHKQDENRKEFRHTSGSYVIGSAHPIKODLFFPAFOHLPAPKOCOFIAHNSRTYGGT	702
Db	651	FHKOSTKINKKFRHISAGIVYGATTTLASDLITPAFCOLFGKORDHFINKRASAYAA5	710
Qy	703	LFFKQSHTLQONYLRLGRAKFSESATIEKPREJPLALDVQSPFSHSDNRMETHYTSLPE	762
Db	711	LHLQHLTLSSPLLRY--LPGSES-----EQPVLFDAQISYIGKNTTKTYTOAPK	761
Qy	763	SEGSMNECINGGIGLDLPFLVLSNPHLPFKTFIQMVEWYVYVONSFFESSD-GGGS	821
Db	762	GESSWYNDGCALIELASSLPHTALSHEGFLPAHVPPIKEASYIHQDSKKEKNTLVTSFD	821
Qy	822	IGRLILNLSIPYGAKFVQGDIDSYTYDLSCGFSDVYRNNPQSTATILVMSDDSKIRGN	881
Db	822	SGDLINVSVPIGIFPERFSRNERASYSBATVIYADVRRKNPDCCTALLINNTSKTTGTN	881
Qy	882	LSRQAFLLRGSNNYYNNSNCELLFGHYAMELWLGSSRNRYVVGTKLRF	928
Db	882	LSRQAGIGIRAGI FYAFSPNLEVTNLSMEIRIGSSRSRYVADLGGGFGQF	928

```

RESULT 5
E86546
polymorphic outer membrane protein G/I family [imported] - Chlamydia pneumoniae (strain 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86546
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tsubuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ida
Nucleic Acids Res. 28, 2311-2316, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A66491; MUID:20330349; PMID:10871362
A:Accession: E86546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <STD>
A:Cross-references: UNIPROT:Q92398; UNIPARC:UPI0000047087; GB:BA000008; NID:g8978819; PI
C:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_9
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match      37.5%; Score 1794; DB 2; Length 928;
Best Local Similarity 42.7%; Pred. No. 3e-93;
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

QY 1 MKTSIPWLVSSVLAFAFSCHLQ----SLANELSPDSSFNGNINSGFTF-----KTSAT 51
DB 1 MKSSLHWFLISSSLALPLSLNPSAFVAVEINLGPNTFSFG--PGYTPPAQTNNADGT 57
QY 52 TYSLTGDVFFYEPGKGTPLSDSCFKQTDNLTFLGNHSLTFGFLDAGTHAGAASTTAN 111
DB 58 IYNLTGDVSIINAGSPTLALTSKCFKETTGNLSFGQHGVQLLQNIADGANC-TETNNAN 116
QY 112 KNLTFSGFSLSPDSSPFTVTYTGQGLSSAGCVNLNIRKLVVAAGNFSTADGAIKAS 171
DB 117 KLSFSGFSYISL--IQTTNATTGGAISKTCAGCSIQGNVSCYFGQNFSDNGALQSS 174
QY 172 FLUTTGSDDALPSNNSSSTKGALITTAGARLANNTGYVFLSNASTSGAIDDEGSI 231
DB 175 ISLS-LNPNLTFYAKKAKATQKGALYSTGTITNNLNSAPSENTAANNAGAIYTEASSF 233
QY 232 LSNNKFLYFEGN---AAKTGGAI-CNTRKASGPELISNNKTLIFASNVAETSGALHA 287
DB 234 ISSNKAISFINNSVYRATSGAIGALICSSSTSAKPVLTISDNGELFIGNTAITSOGAIYT 293
QY 288 KKLALSSGGFTFELRN--VSSATPKGAISIDASGELISLAETGNITFVRNTLT-TT-IGST 345
DB 294 DNLVSSGGPFLTKNNSAIDTAAPIGGAIAIADSGSLISALGDIITEGNTVVYVGAASS 353
QY 346 DTPKKNALINIG-SNGKFTFLRAAKNHTTFYDPTPISEGTS--SDVLKIKNNSAGALNYQ 402
DB 354 OTTTSNINIGNTANKIVQLRASQGNITVFDPITTSITTAALSDALNINGPDLGNPAYQ 413

```

[illegible]

```

RESULT 6
G86546
polymorphic outer membrane protein G family [imported] - Chlamydomonas pneumoniae (strain
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86546
Rishiara, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Iet
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; PMID:20330349; PMID:10871362
A:Accession: G86546
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <STO>
A:Cross-references: UNIPROT:Q9RB65; UNIPARC:UPI000002PFF0; GB:BA000008; MID:g8978821; PII
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_10
C:Superfamily: Chlamydomonas pneumoniae polymorphic outer membrane protein G

Query Match          37.3%; Score 1785; DB 2; Length 928;
Best Local Similarity 40.4%; Pred. No. 9.5e-93;
Matches 385; Conservative 173; Mismatches 344; Indels 52; Gaps 18;

QY      1 MKTSPWLVSVLA--FSCHQLSLANEILSPDPSFNGISDGTTPKTSAT--TVSLT 56
       |||:::|||||||::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 MSQSFWLVLSTLACFTSCSTVFAATAENIGSDSPDGSTNTGTVPKNATTGIDVTLT 60

QY      57 GDVFPEPGKGTPLSDCFKQTNDITFLANGSLTGFIDAGTHGAALSTANKULT 116
       |||:::|||||||::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 GDTITONLDSDAALTGKCFSDDTESLSFACKGYSLPLINKSSAE-GAASVTYDKNLST 119

QY      117 SGEFSLSPSSPBTWT--GGCTLSAGGVNLEIRKLVAAGFNADGAIKASPL 174
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      120 TGSSSLTFPAARBSVTTTSGKAVKCGDLTFDNNGTILPKDYCYEENGAIATKINSL 179

```

QY 175 TGTSGDALFSSNNSST---KGAIAATTAGARIANTGYVRFLSNIASTSGAIDDEGTST 231
 Db 180 KNSTGSIISFEGKSSATGKKGALCATGYVDITNNTPFLFSNNIAEAGAINSTGNC 239
 QY 232 LSNKKFLYFEGNAKATT---GGAICNTKASGSPBELIISNNKTLIFASNAETSGAIIHAK 288
 Db 240 ITGNTSLVFSSENSVYATAGNGAL-----SGDADVTISNQSVTFSGNQAVANGAIIYAK 294
 QY 289 KALSS--GGFTEPLANNVSATP--KGAISIDASGELSIAETGNTTFPRNLTITGST 345
 Db 295 KLTLASGGGGGISFSNNIVGTTAGNGAIIISILAEBCSLSAEAGDITFEGNAIVAT-TP 353
 QY 346 DTPKRNAINISNGKFTLEPRAKNHTIFFYDPIITSE--GTSSDVLKINNSAGALNPYOG 403
 Db 354 QTKRNSIDIGSTAKITNLRAISGHSIFFYDPIITANADSTDLINAKADAGNSTDYG 413
 QY 404 TILFSGETLTADLKVADNLKSSFTQPVSLSGCKLLQKGVTLBSTSFSQAGSLGMDS 463
 Db 414 SIVFSGEKLSEDEAKVADNLSTLKQPVTLTAGNLVLRKGVTLDTKGFQTAGSSVIMDA 473
 QY 464 GTTLSTTAGSITTLNGLINVDISGLKOPVSLTAKGANSKVIYSGKNTLIDIEGNIYESHM 523
 Db 474 GTTLKASTEBEVTLTGLSIPVDSLGEKGVVIAASAKRNVALSGPILLDNQNAIYEND 533
 QY 524 FSHDQLFSLKITVDADVDTNVDISLIPVPAEDPNSEYGFQOGOMNVNMTTDTAT--NTK 581
 Db 534 LGKTODFSFVQLSA-LGTATTTDVPA---VPYATPPTHYGOGTGMGTWVDDTASIPKTK 589
 QY 582 EATATWTKTGVPVSPERKALVONTLMGVFTDIRSLQOLVEIGATGMEHKQGFWSSMTN 641
 Db 590 TATLAWTNTGYLPPNERQGPLVPNSLWGSFSDIOAIGVIERAALTLCSDRGFWAGVAN 649
 QY 642 FLHKTGDENRKGRPHHSAGVIVGSAHTPKDDLFTPAFCHLFAARDCEFIANNHNSRYGG 701
 Db 650 FLDKDKKGRKRYRHRHSGGYAIGAAQTCSENLISFAFCQLFSDSDKPLVAKNHTDYAG 709
 QY 702 TLFFKSHHTLOPONYLRLGRAKFSESAIEKFP---REIPLADVOVSFSSDNRMETHYT 758
 Db 710 APLFIQHTTEC-----SGFICGLDLKLGSMHKLPLVLEGQALVHVSNDLTKYTT 759
 QY 759 SLPESEGSWSNECIAGIGLDLPVLSNPH---LEKTFIPQMKVEMVYVQNSFEFESS 814
 Db 760 AYEPEVSGSWGNNAFNNMLGAS-----SHSYPEYLHCFDYAPYIKLNLTYIRQDSFESEK 814
 QY 815 SDGRGFSIGLNLSTIVGAKFVQGDIGSYTYDLSGFVSDVYRNNPOSTATLWNSPDS 874
 Db 815 TEGRSFSDSNLFLNLSLPIGVKFEKFSDCNDFSVDLTLSYVPDLIRNDPKCTTALVSGAS 874
 QY 875 WKIRGGLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNNYNDVGTCKLRF 928
 Db 875 WEYIANNLARQALQVRAGSHYAFSPMEFVLGQFVEVRGSSRIYNDLGKRFQF 928

RESULT 7
 G81591
 polymorphic membrane protein G family CP0303 [imported] - Chlamydia pneumoniae (stra
 C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: G81591
 R/Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dodgen, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A/Title: Genome sequences of Chlamydia trachomatis Morn and Chlamydia pneumoniae AK39.
 A/Reference number: AB1500; MUID:2015025; PMID:10684935
 A/Accession: G81591
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-928 <REA>
 A/Cross-references: UNIPROT:Q9RB65; UNIPARC:UP1000002FFFO; GB:AE002192; GB:AE002161; NIT
 A/Experimental source: strain AK39, HL cells
 C/Genetics:
 A/Gene: CP0303

C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match	37.3%	Score 1785;	DB 2;	Length 928;
Best Local Similarity	40.4%	Pred. No. 9.5e-93;		
Matches	385;	Conservative 173;	Mismatches 344;	Indels 52; Gaps 18;

QY 1 MKTSLPWLVSVA--FSCHLOSANBELSPDPSFNGNIDSGTFPTSAT--TYSIT 56
 Db 1 MKSQFSLWVLSLACFTGCSITVPAATANIPEPSDFDSTMTGVTTPKNTTGTGIDYTLT 60
 QY 57 GDVFFEPGKGTPLSCKKQTTDNLTPNGHSLTFGIDAGTAGAALASTANKULF 116
 Db 61 GDTITQNLDSALRTGCFSDTTESLSFAGKYSLSFNIKSAE--GAALSVTTDNLEL 119
 QY 117 SGFSLSPDSPTTYT--GGTSLSAGVNLNRLVWAGNFSTADGAIKGAFL 174
 Db 120 TGFSSLTFLAAPSVTITPSGKAYCGDILFDNNGTILFKODYEEBNGAISTGNLSL 179
 QY 175 TGTSGDALFSSNNSST---KGAIAATTAGARIANTGYVRFLSNIASTSGAIDDEGTST 231
 Db 180 KNSTGSIISFEGKSSATGKKGALCATGYVDITNNTPFLFSNNIAEAGAINSTGNC 239
 QY 232 LSNKKFLYFEGNAKATT---GGAICNTKASGSPBELIISNNKTLIFASNAETSGAIIHAK 288
 Db 240 ITGNTSLVFSSENSVYATAGNGAL-----SGDADVTISNQSVTFSGNQAVANGAIIYAK 294
 QY 289 KALSS--GGFTEPLANNVSATP--KGAISIDASGELSIAETGNTTFPRNLTITGST 345
 Db 295 KLTLASGGGGGISFSNNIVGTTAGNGAIIISILAEBCSLSAEAGDITFEGNAIVAT-TP 353
 QY 346 DTPKRNAINISNGKFTLEPRAKNHTIFFYDPIITSE--GTSSDVLKINNSAGALNPYOG 403
 Db 354 QTKRNSIDIGSTAKITNLRAISGHSIFFYDPIITANADSTDLINAKADAGNSTDYG 413
 QY 404 TILFSGETLTADLKVADNLKSSFTQPVSLSGCKLLQKGVTLBSTSFSQAGSLGMDS 463
 Db 414 SIVFSGEKLSEDEAKVADNLSTLKQPVTLTAGNLVLRKGVTLDTKGFQTAGSSVIMDA 473
 QY 464 GTTLSTTAGSITTLNGLINVDISGLKOPVSLTAKGANSKVIYSGKNTLIDIEGNIYESHM 523
 Db 474 GTTLKASTEBEVTLTGLSIPVDSLGEKGVVIAASAKRNVALSGPILLDNQNAIYEND 533
 QY 524 FSHDQLFSLKITVDADVDTNVDISLIPVPAEDPNSEYGFQOGOMNVNMTTDTAT--NTK 581
 Db 534 LGKTODFSFVQLSA-LGTATTTDVPA---VPYATPPTHYGOGTGMGTWVDDTASIPKTK 589
 QY 582 EATATWTKTGVPVSPERKALVONTLMGVFTDIRSLQOLVEIGATGMEHKQGFWSSMTN 641
 Db 590 TATLAWTNTGYLPPNERQGPLVPNSLWGSFSDIOAIGVIERAALTLCSDRGFWAGVAN 649
 QY 642 FLHKTGDENRKGRPHHSAGVIVGSAHTPKDDLFTPAFCHLFAARDCEFIANNHNSRYGG 701
 Db 650 FLDKDKKGRKRYRHRHSGGYAIGAAQTCSENLISFAFCQLFSDSDKPLVAKNHTDYAG 709
 QY 702 TLFFKSHHTLOPONYLRLGRAKFSESAIEKFP---REIPLADVOVSFSSDNRMETHYT 758
 Db 710 APLFIQHTTEC-----SGFICGLDLKLGSMHKLPLVLEGQALVHVSNDLTKYTT 759
 QY 759 SLPESEGSWSNECIAGIGLDLPVLSNPH---LEKTFIPQMKVEMVYVQNSFEFESS 814
 Db 760 AYEPEVSGSWGNNAFNNMLGAS-----SHSYPEYLHCFDYAPYIKLNLTYIRQDSFESEK 814
 QY 815 SDGRGFSIGLNLSTIVGAKFVQGDIGSYTYDLSGFVSDVYRNNPOSTATLWNSPDS 874
 Db 815 TEGRSFSDSNLFLNLSLPIGVKFEKFSDCNDFSVDLTLSYVPDLIRNDPKCTTALVSGAS 874
 QY 875 WKIRGGLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNNYNDVGTCKLRF 928
 Db 875 WEYIANNLARQALQVRAGSHYAFSPMEFVLGQFVEVRGSSRIYNDLGKRFQF 928

RESULT 8
 D86546

polymorphic outer membrane protein G family [imported] - Chlamydia pneumoniae (strain
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C/Accession: D86546
R/Shitai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A/Reference number: A86491; MUID:20303049; PMID:10871362
A/Accession: D86546
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-930 <STO>
A/Cross-references: UNIPARC:UPI00001655FB; GB:BA000008; NID:98978818; PIDN:BAA9654.1; G
A/Experimental source: strain J138
C/Genetics:
A:Gene: pmp 8
C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 36.9%; Score 1763; DB 2; Length 930;
Best Local Similarity 41.7%; Pred. No. 1.6e-91;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

QY 1 MKTIPVAVSVLAFCCHLOSLAN---EELSPDDSPNGNIDSGTFPTKSA---TTY 53
DB 1 MKTIPVAVSVLAFCCHLOSLAN---EELSPDDSPNGNIDSGTFPTKSA---TTY 53
QY 54 SLTGDVFEYBPKGTPLSDSCFKQTTDNLTFLGNHSLTFEGIDAGTHAGAASTTANKN 113
DB 59 VLSGNVYINDAGKGTALTGCCFTETTGDLTFGTGYSFSPFTVAGSNAGAASTADKA 118
QY 114 LTFSGFSLSPDSSPTVTVTGQTLSSAGVNLNIRKLVVAGNFSTA---DGAIKGA 170
DB 119 LTFGFSNLSPFIAPGTTVAGSKSTLSAGALNLTNGDTILFSGVNSNEANNNGAITAK 178
QY 171 SFLITGSGDALFSNNSSSTKGAIATTAGRIANNNGYVFLSNASTSGAIDDEGTS 230
DB 179 TLTSGNTSSITFTSNKAKKLGAIYSSAAASISGNTGQLVFNNKGETGGALGFPASS 238
QY 231 ILSNNKFLYEGNAKKT---GGAICNTKAGSPELIISNNKTLIPASNVATSGAIIHA 287
DB 239 SITONSSILFSGNATTAAGKGAIIYCEKTEPTLTISGNKSLTFEANSVTOGGAIICA 298
QY 288 KKLALSSGCFTEFLRNNV--SSATPKGAIISIDAGELSLAETGNITFVNTLTGSTD 346
DB 299 HGLDLASAAGPTLFSNNRCGNTAAGKGAIIADSGSLSLSANOGDITFLGNTLTST--SAP 357
QY 347 TPKRNAINISNGFTELRANKHTTIPYDPTSEGT--SSDVLIKNNGSAGALNPYQGTI 405
DB 358 TSTNNAIYLSSAKITNLRAAGOSIIFYDPIASNTTGASDVLTIPODSSPLDYSGTI 417
QY 406 LFSGETTLADELKVADNLSKSFQTVPSLSGGKLLLOKGVTLSESTFSQEAAGSLGMDSGT 465
DB 418 VFSGEKLSADEKAKADNFTSLIKQPLALASGTLAKGNVELDVNGFTOTEGSTLLMQPQT 477
QY 466 TLTSTAGSITTTNLGINVDSLGLKQPVSLTAKGASNKIYVSGKLNLDIEGNIYESHMF 525
DB 478 KKLADTEAISLTKLVDLSALEGNKSVSIEFAGANKITLTLSPIVFGQSSGNFESHRTI- 536
QY 526 HDQFLSL-LKTTVDADVDTNVDISLIVPAEDPNSEVFGQGNQVNTTDTATNTKEAT 584
DB 537 -NQAFTQPLVVFATAATAADYIDALTLTSPVQTEPHYQOGHWEATW-ADTST--AKSGT 593
QY 585 ATMTKGTVPSPERSALVONTLMGVFTDIRLSLOOLVEIGATGMHKGQFVWSNUNLH 644
DB 594 MTWATTGNPNPERASVVPDLSMASFTDIRLQOIMTSQANSIYQOGLAASGTANFFH 653
QY 645 KTGDENRKGFPHTSGGVYIGSAAHTPKDGLTFPAFCHLFARDKOCFIANNSTRYGGTLF 704
DB 654 KDKSGTNAFAFRHKSIGYIVGSAEDFSENISFVAICQLFGKDKOLFIEYENTSHVNLASTLY 713
QY 705 FKHSHHTLOPQVNLIRGAKFSESAIEKFPREIPLADVQVSFSDNEMETHYSLPSE 764
DB 714 LQHRAFLG-----GLPMPSPFGSITDMLKDIPILINAQLSYSTKNDMDRRYTSYPEAQ 766

polymorphic outer membrane protein G family CP0307 [imported] - Chlamydia pneumoniae (strain
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: A81591
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: A81591
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-930 <REA>
A/Cross-references: UNIPROT:Q9Z393; UNIPARC:UPI00001655FB; GB:AE002193; GB:AE002161; NID:
A/Experimental source: strain AR39, HL cells
C/Genetics:
A:Gene: CP0307
C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 36.9%; Score 1763; DB 2; Length 930;
Best Local Similarity 41.7%; Pred. No. 1.6e-91;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

QY 1 MKTIPVAVSVLAFCCHLOSLAN---EELSPDDSPNGNIDSGTFPTKSA---TTY 53
DB 1 MKTIPVAVSVLAFCCHLOSLAN---EELSPDDSPNGNIDSGTFPTKSA---TTY 53
QY 54 SLTGDVFEYBPKGTPLSDSCFKQTTDNLTFLGNHSLTFEGIDAGTHAGAASTTANKN 113
DB 59 VLSGNVYINDAGKGTALTGCCFTETTGDLTFGTGYSFSPFTVAGSNAGAASTADKA 118
QY 114 LTFSGFSLSPDSSPTVTVTGQTLSSAGVNLNIRKLVVAGNFSTA---DGAIKGA 170
DB 119 LTFGFSNLSPFIAPGTTVAGSKSTLSAGALNLTNGDTILFSGVNSNEANNNGAITAK 178
QY 171 SFLITGSGDALFSNNSSSTKGAIATTAGRIANNNGYVFLSNASTSGAIDDEGTS 230
DB 179 TLTSGNTSSITFTSNKAKKLGAIYSSAAASISGNTGQLVFNNKGETGGALGFPASS 238
QY 231 ILSNNKFLYEGNAKKT---GGAICNTKAGSPELIISNNKTLIPASNVATSGAIIHA 287
DB 239 SITONSSILFSGNATTAAGKGAIIYCEKTEPTLTISGNKSLTFEANSVTOGGAIICA 298
QY 288 KKLALSSGCFTEFLRNNV--SSATPKGAIISIDAGELSLAETGNITFVNTLTGSTD 346
DB 299 HGLDLASAAGPTLFSNNRCGNTAAGKGAIIADSGSLSLSANOGDITFLGNTLTST--SAP 357
QY 347 TPKRNAINISNGFTELRANKHTTIPYDPTSEGT--SSDVLIKNNGSAGALNPYQGTI 405
DB 358 TSTNNAIYLSSAKITNLRAAGOSIIFYDPIASNTTGASDVLTIPODSSPLDYSGTI 417
QY 406 LFSGETTLADELKVADNLSKSFQTVPSLSGGKLLLOKGVTLSESTFSQEAAGSLGMDSGT 465
DB 418 VFSGEKLSADEKAKADNFTSLIKQPLALASGTLAKGNVELDVNGFTOTEGSTLLMQPQT 477
QY 466 TLTSTAGSITTTNLGINVDSLGLKQPVSLTAKGASNKIYVSGKLNLDIEGNIYESHMF 525

478 KKKDTEAISTLKTVVDDLSALEGKNSVSIETRAGANKTITLTSPLVFPQSSGNFIESHTI - 536

QY 526 HDOLFSL-LKLTIVDADVDTNVDISSLIIPVPAEDPENSEYGFQGMVMVMTTDTATVTKCAT 584

Db 537 -NQATQGLVLPYTAATAASDIYIDLLTSPVQOTPERPHYIGQGHMAYT-ADTST-AKSGT 593

QY 585 ATWTKTGFVSPBERKSALVCMTLMGVFTDIBSLQOLVEIGATGMEHKOGFWVWSMTNLEH 644

Db 594 MTWVTYTGVPNPNBERASVYPDSLMSFTDIRLQOIMTSQANSIYQOGIWMASGRANFEH 653

QY 645 KTGDENRKGFRHTSGGYIIGSSAHTPKDDLFTFAFCHLPARDKCFIAHNSRYGTGLF 704

Db 654 KDKSGTNGAFRRKHSYGYIVGGSABDPSENIIFSVCQJFGKDKOLFIVENTSHNYLASTLY 713

QY 705 FKHSHTLOPQNYVLRIGRAKFSESALIEKPPREIPLADVQVSEFSHSDNEMETHYISLPSE 764

Db 714 LQHRFAFG-----GLMPFSFGSITDMLKDPIILNMQLSYSYKNDMDRTYTSYPAQ 766

QY 765 GMSMSECTIAGIGLDLPFVLSNPHLPFTFPIPMKVMENVYYSQNSFFPSSSDGRCGFSIGR 824

Db 767 GSWTNNSGALIEIGGSLATYLPKEARPFQGYPPFLFKQAVYRQQNFKESGAEARAFDDGD 826

QY 825 LLNLSTIPGAKFVQGDIGDSTYYDLSGFFVSDVYANNQSTAITLYMSDPMKIRGNLSR 884

Db 827 LVNCSIPVIGIRLEKISBEDEKNNFEISLAVYIGVYAKNRSRTSLMWSGASWTSLCKNLAR 886

QY 885 QAFLLRGSNNVYVNSNCFLPGHYAMELRGSSNNVYVDTCLRF 928

Db 887 QAFILASGSHLTLSPHVELSGEAAAYELRGASHIYVVDGLGYSF 930

```

RESULT 10
D72078
polymorphic outer membrane protein g family - Chlamydomophila pneumoniae (strain CW1029)
C:Species: Chlamydomophila pneumoniae, Chlamydomophila pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: D72078
R:Katzman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J., et al.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72078
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-930 <ARN>
A:Cross-references: UNIPROT:Q9Z393; UNIPARC:UP1000004708C; GB:AE001627; GB:AE001363; NII
A:Experimental source: strain CW1029
C:Genetics:
A:Gene: pmp_8
A:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match          36.8%; Score 1761; DB 2; Length 930;
Best Local Similarity 41.7%; Pred. No.2,1e-91;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

QY      1 MKTSPWLVSSVIAFSCHLOSLAN--EELISPDSPFNIGDSTPTPKTSA---TTY 53
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MKIPHLKLLISTVLTPI-LLSIATYVGADASISPTDSPDG-AGSGTTPPKSTADANGTNY 58
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      54 SLTGDFEYFBQKGTPLSDSCFQKTTDNLTFLGNHSLTFPIDAGTHAGAASTTANKN 113
      54 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      59 VLSGNVYINDAGKGTALGCCFTETTGDTLITGKCYSSFTVVDGNSVAGAASTTADKA 118
      59 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      114 LTFSGFSLSPDSSPTVTVTGGCTLSSAGAGVNLNIRKLVVAGNFSTA--DGGAIKGA 170
      114 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      119 LTFTFSNLSFIAAGCTTAVASGKSTLSAGAILNLTDNGTILFSGQVNSEAANNNGAIPTK 178
      119 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      171 SPFLTGSGDALFSNNSSSTGGAATATAGARIANNCTGYAFLNSIASTSGAIDDECTS 230
      171 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      179 TLISIGNTSITFTFSNSAKKLGALYSAAASISGNTQQLVPMNNKGTGGALGFEASS 238
      179 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      231 TLSNNKFLYFEGNAAKT---GGAICNTKASGPELIIINNKTLLIPASNAVETSGAIIHA 287
      231 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 239 SITONSSLEFSGNATDAAGKGAICYCEKTGEFTPLTISGNKSLTPRENSVYOGAICA 298
Qy 288 KKLALSSGGFEFFLRNVV-SSATPKGGAISIDASGELSLSAETGNITFVNTLITTTGSTD 346
Db 289 HOLDLISAAGPLFPSNNRCGNTAAKGGAIAIADSGSLISANOGDITPLNGLTIST-SAP 357
Qy 347 TPKRNAINGSNCKFTELPAAKNHTIEFYDPLTSEGT-SSDYVKINNGSAGALNPYGTI 405
Db 358 TSTRNAIYGSAAKTNLPLAAGOSIYFYDPLASNTTASDVLTINOPDSNPILDYGTI 417
Qy 406 IFSGETLTADDELKVDNMLKSSFTQPVLSGSKLLQKGYLTJESTSPSOEAGSLIGMDST 465
Db 418 VFSGEKLSADKAAKNDFSTILKQPLALASGTLALKGNVELDVNGVFTQTEGSLTLMQPGT 477
Qy 466 TLSTAGSTTTNLGINVDSLGIKQPVSLTAGASKNVIVSGKLNLDIEGNIYESHMFS 525
Db 478 KKKADTEALSTLKLVDLDSALGKNSVSIETMANNTITLTSPLVPDSSGNFYESHTI- 536
Qy 526 HDQLFSL-LKITVDDVDVDTNVDISSLIPVAEPDPNSEYGFQGGOMVNMVMTDTATNTEAT 584
Db 537 -NQATQPLVFTTAATAADIIYIDALLTSPVQTEPBEHYIGOGMEATW-ADTST-AASGT 593
Qy 585 ATWYKTFEVPSPERKSALVCNTLMGVFTDIRSIQOLVEIGATGMEHKQGFVWSSMTNPLH 644
Db 594 MTWVTGVYNNPERRASVVPDSIMASFTDIRTQQMTSQAANSIYOQRGILMASTANFPH 653
Qy 645 KTGDENRKGFRTSGGYVIGSAAHTPKDDLPTFAFCHLPARDDCFAHNNSRTYGGTLF 704
Db 654 KDKSGTNQAFRIKSGYIYIGSSHEDSENI FSAFQOLRGKDXDLFVEMTSHNYLASLY 713
Qy 705 FKHSHTLQONYLRLGRAKFSESAIEKFPREIPLADVQVFSFSDNRMETHYTLSESE 764
Db 714 LQHRAPFLG-----GLPWPSPGSIIDMKDIPILINAQLSYSYTKNDMDTRYTSYDEAQ 766
Qy 765 GMSNECTIAGGIGLDLPFLSNPHPLFKTFPIPMKXEMVYVSGNSPFESSDDGGEFSTGR 824
Db 767 GSWTNNSGALTELGGSLATYLPKEAPFFQGYFPLFKQAVYSRQONFESGAGEAALPFDGD 826
Qy 825 LNLNLSIPVGAKEVQGDIDGSIYTYDLSGFPVSDVYRRNPNPOSTATLWNSPDSMKIRGMLSR 884
Db 827 LVNCSIPVQIRLEKXISBDEKKNFETISLAYIGDYRRKNPSRSTLWNSGAWMTSLCKNLAR 886
Qy 885 QAFLLRGSNNVYVNSCELFGHYAMELRGSSRRNVYDVGTCLRF 928
Db 887 QAFLLASAGSHLTLSPHVELSGEAAVELRGSAAHLYYNDVCGIRYVF 930

```

```

RESULT 11
C72078
polymorphic outer membrane protein g family - Chlamydomophila pneumoniae (strain CWL029)
C.Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C.Accession: C72078
R.Katman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A.Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A.Reference number: A72000; MUID:99206606; PMID:10192388
A.Accession: C72078
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-936 <ARN>
A.Cross-references: UNIPROT:Q9Z898; UNIPARC:UPI00000470BC; GB:AE001627; GB:AE001363; NID:
A.Experimental source: strain CWL029
C.Genetics:
A.Gene: pmp_7
C.Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match      36.3%; Score 1734; DB 2; Length 936;
Beet Local Similarity 39.9%; Pred. No. 7, 2e-80;
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

1 MKTSLPWLAVSSVLAFSCHLQSLANEELLSPDPSFNGNIDSGTF-----TPKTSATTYSL 55
|||||

```

Db 1 MKSSVSWLFFSSIPLEFSSLSIYAAEVLTLDSNNNSYDGS--NGTTFVFTSTDDAAAGTTYSL 59
Qy 56 TGVVFVEBPK-GTPLSDSCFKQTTDNLFLNGHSLTFPGIDAGTHAGAASTT-ANKN 113
Db 60 LSDVSFQNGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSAGVASTADKN 119
Qy 114 LTFSGFSLSPDSSPTTYT-TQGTLSAGVNLLENIRKLVVAGNFTADGAIKASAF 172
Db 120 LTFNDFRLSLISICPFLSLSPGQCALKSVGNLSLTGNSQIIFQNFSNDNGVINTKNF 179
Qy 173 LLTGSGDALFSNNSSST--KGAIAITTAGARIANNNGYRFLSNLSTSGAIDDEGTS 230
Db 180 LLSGTSQFASFSRNQAFGTGQGVVATGTTTENSIGIVSFSONLAKSGGALYSTDNC 239
Qy 231 ILSNNKFLYFEGN---AAKTGGAI CNTKASGPELII SNKTLIFASNVAETSGAII 286
Db 240 SITDNFOVIFDGNASAMEAQAOGAICCTTTDKT--VTLGNKSLSTNNLTALTYGAIS 297
Qy 287 AKKLALSSGCFTEFLRNNSATP---KGAISIDAGELSLSAETGNITFVNTLTITG 343
Db 298 GLKVISIAGGPTLF-QSNISGSSAGGGGAINIASGELALSTSGDITF-NNNQVTNG 355
Qy 344 STDPKRNAINISNGKFTFLRAAKNHTIFFYDPTISEGT--SSDYUKINNGSAGALNPY 401
Db 356 STST--RNAINITDIAKVISIRAAFGOSIYFYDITPMTAASDTLNLNLADANSIEY 413
Qy 402 QGTILFSGETLTADLKVADNLKSFQPVLSGGKLLQKVLTLESTSFQEAAGSLGM 461
Db 414 GGAIVFSGEKLSPEKAIANVTSTIQPVLARGDLVLRGVVTVTKDLTQSGSLIM 473
Qy 462 DSGTTLSTAGSITITNLGINVDSLGLQPVSLTAKAGSNKVIKGLNIDIEGNITYS 521
Db 474 DGGTTLTSAKEANLSLNGLAIVLSLDGNTKALKTEADKNISLSGTIALIDTEGSEYEN 533
Qy 522 HMFHDQLFSLKLTVDADVNDVNDISLIPVPAEDPNSSEYFGQGNVNMVTTDTANTK 581
Db 534 HNLKASATYPLLELT-AGANGTITLALSTLTLQEBETHYQGNQOLSWA--NATSSK 590
Qy 582 EATATWTKGVFVSPERKSALVCTNLWGVPFDIRSLQOLVEIGATGMEHKQGFVWSMTN 641
Db 591 IGSINMTRTGYIIPSPERKSNLPLNSLMGNFIDIRSIQLITKSSGEPFERELMLSGIAN 650
Qy 642 FLHKTGDNKGRFRRHSGVIGGSAHTPKDCLTFPACHLFAKDCCFLAHNNSRTYGG 701
Db 651 FFYRDSMPTRHGRHISGGYALGITATTAPADQLTFPACQLFARDRNHITGKNHDTYGA 710
Qy 702 TLFKHSHTL-QPQNYLRLGAKSESIAIEKPREIPLADVOVYFSSIDNRMTHTYSL 760
Db 711 SLVYHHTEGFLDIANFL-WGKATRAPVWLSISQIILPSFPAKFSYLHTDMMKTYTIDN 769
Qy 761 PESGWSNNECIAGIGLGLPFLVLSNPHPLFKTFIPQMKVEMVYVSONSFESSSDGRGF 820
Db 770 SIIRGSRNDAFCADLGASLFPVIVSVY-LKKEVFPVKQVYIYAHQODFYERAAEGRAF 828
Qy 821 SIGRLNLISIPVGAKFVQGDIGDSYTYDLSGFVSDVYRNNPQSTATLWMSPDWKIRGG 880
Db 829 NKSELINVEIPIGTFFERDSKSEKGTYDILMYILDAVRNPKCQTSIIASDANMMAVGT 888
Qy 881 NLSQAFLRGSNNVYVNSCELFGHYAMELRGSSRRNVVVGRTKLP 928
Db 889 NLAQGFVRAANHPQVNPMEIFQGFAPFEVRSRRNNTNLGSKPCF 936

RESULT 12

B81591
polymorphic membrane protein G family CP0308 [imported] - Chlamydia pneumoniae (stra
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: B81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonev, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A:Reference number: B81500; MUID:20150255; PMID:10684935
A:Accession: B81591
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-936 <REA>
A:Cross-references: UNIPROT:Q92898, UNIPARC:UPI000013ICD, GB:AE002193, GB:AE002161, NID:
A:Experimental source: strain AR39, HL cells
C:Genetics:
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G
Query Match 36.2%; Score 1733; DB 2; Length 936;
Best Local Similarity 39.9%; Pred. No. 8.2e-90;
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

Qy 1 MKTISPMVWLVSSVLAFCSLQIANEELSPDSSFNGNIDSGT-----TPKTSATTYSL 55
Db 1 MKSSVSWLFFSSIPLEFSSLSIYAAEVLTLDSNNNSYDGS--NGTTFVFTSTDDAAAGTTYSL 59
Qy 56 TGVVFVEBPK-GTPLSDSCFKQTTDNLFLNGHSLTFPGIDAGTHAGAASTT-ANKN 113
Db 60 LSDVSFQNGALGIPLASGCFLEAGGDLTFQGNQHALKFAFINAGSAGVASTADKN 119
Qy 114 LTFSGFSLSPDSSPTTYT-TQGTLSAGVNLLENIRKLVVAGNFTADGAIKASAF 172
Db 120 LTFNDFRLSLISICPFLSLSPGQCALKSVGNLSLTGNSQIIFQNFSNDNGVINTKNF 179
Qy 173 LLTGSGDALFSNNSSST--KGAIAITTAGARIANNNGYRFLSNLSTSGAIDDEGTS 230
Db 180 LLSGTSQFASFSRNQAFGTGQGVVATGTTTENSIGIVSFSONLAKSGGALYSTDNC 239
Qy 231 ILSNNKFLYFEGN---AAKTGGAI CNTKASGPELII SNKTLIFASNVAETSGAII 286
Db 240 SITDNFOVIFDGNASAMEAQAOGAICCTTTDKT--VTLGNKSLSTNNLTALTYGAIS 297
Qy 287 AKKLALSSGCFTEFLRNNSATP---KGAISIDAGELSLSAETGNITFVNTLTITG 343
Db 298 GLKVISIAGGPTLF-QSNISGSSAGGGGAINIASGELALSTSGDITF-NNNQVTNG 355
Qy 344 STDPKRNAINISNGKFTFLRAAKNHTIFFYDPTISEGT--SSDYUKINNGSAGALNPY 401
Db 356 STST--RNAINITDIAKVISIRAAFGOSIYFYDITPMTAASDTLNLNLADANSIEY 413
Qy 402 QGTILFSGETLTADLKVADNLKSFQPVLSGGKLLQKVLTLESTSFQEAAGSLGM 461
Db 414 GGAIVFSGEKLSPEKAIANVTSTIQPVLARGDLVLRGVVTVTKDLTQSGSRILM 473
Qy 462 DSGTTLSTAGSITITNLGINVDSLGLQPVSLTAKAGSNKVIKGLNIDIEGNITYS 521
Db 474 DGGTTLTSAKEANLSLNGLAIVLSLDGNTKALKTEADKNISLSGTIALIDTEGSEYEN 533
Qy 522 HMFHDQLFSLKLTVDADVNDVNDISLIPVPAEDPNSSEYFGQGNVNMVTTDTANTK 581
Db 534 HNLKASATYPLLELT-AGANGTITLALSTLTLQEBETHYQGNQOLSWA--NATSSK 590
Qy 582 EATATWTKGVFVSPERKSALVCTNLWGVPFDIRSLQOLVEIGATGMEHKQGFVWSMTN 641
Db 591 IGSINMTRTGYIIPSPERKSNLPLNSLMGNFIDIRSIQLITKSSGEPFERELMLSGIAN 650
Qy 642 FLHKTGDNKGRFRRHSGVIGGSAHTPKDCLTFPACHLFAKDCCFLAHNNSRTYGG 701
Db 651 FFYRDSMPTRHGRHISGGYALGITATTAPADQLTFPACQLFARDRNHITGKNHDTYGA 710
Qy 702 TLFKHSHTL-QPQNYLRLGAKSESIAIEKPREIPLADVOVYFSSIDNRMTHTYSL 760
Db 711 SLVYHHTEGFLDIANFL-WGKATRAPVWLSISQIILPSDADFSLHTDMMKTYTIDN 769
Qy 761 PESGWSNNECIAGIGLGLPFLVLSNPHPLFKTFIPQMKVEMVYVSONSFESSSDGRGF 820
Db 770 SIIRGSRNDAFCADLGASLFPVIVSVY-LKKEVFPVKQVYIYAHQODFYERAAEGRAF 828
Qy 821 SIGRLNLISIPVGAKFVQGDIGDSYTYDLSGFVSDVYRNNPQSTATLWMSPDWKIRGG 880

Db 829 NKSELINVEITIGTTFEEDSKSEKGYDTULTIMYLIDARRRPRKQOTSLASDANMAVGT 888

Qy 881 NLSFOALFLRGSSNNVYVNSNCELFQHYAMELRGSSRRNVVDVGTKLRF 928

Db 889 NLAHQGFSEVRANHFQVNPHEIRFGQFAFEVRSSRRNVNTLQSGKFCF 936

RESULT 13

C86546

polymorphic outer membrane protein G family [imported] - Chlamydomophila pneumoniae (strain C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C:Accession: C86546 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ida, A.: Nucleic Acids Res. 29, 2311-2314, 2000 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J13.8. A:Reference number: A86491; MUID:20330349; PMID:10871362 A:Accession: C86546 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-936 <STO> A:Cross-references: UNIPROT:Q9Z898; UNIPARC:UPI0000131CED; GB:BA000008; NID:g8978817; P:Experimental source: strain J138 C:Genetics: A:Gene: pmp-7 C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match 36.2%; Score 1733; DB 2; Length 936;

Matches Local Similarity 39.9%; Pred. No. 8.3e-90; Mismatches 35; Indels 32; Gaps 18;

Db 1 MKSTIPWLVSSVAFSCHQSLANEBLSPDPSFNGIDSGT-----TPKTSATTYSL 55

Qy 56 TGDVFEYEPKQ-GTPPLSDSCFKQTTDNITPLGNGHSLTFGTIDAGTHAGAASTT-ANKN 113

Db 60 LSDVSFOVAGLGIPIPLASGCFLEAGDGLTFQGNHALLFAFINAGSSAGTVAASDAKN 119

Qy 114 LTFVGFSLSPDSSPTVT--TGQGLSSAGVLENIRKLVVANGSTADGCAIKGASF 172

Db 120 LTFVDFSLSLISCPSLSPGOCALSSVGNLSLTGNSQITLIPONTSSDGVYINTKPF 179

Qy 173 LLTGSGDALSSNNSSST--KCGAIAATTAGARIANNVGYFLSNISTSGAIDDEGTS 230

Db 180 LLSGTSGQASFSRNOAFQKQGGVYVANGTITTIENSPOIVFSGNLAKGSGALYSTDC 239

Qy 231 ILSNNKFLYPEGN---AAKTGGALCNTKASGSELIISNNKTLIPASNAVETSGGAIH 286

Db 240 SITDNFYQIFDGNASMEAOAGGALCCTTIDKT--VTLGNKMLSPNNNTALTYGALIS 297

Qy 287 AKKLALSSGGTFEFLRNVSATP---KGAISIDASELSLSAETGNIITVRYTLTTTG 343

Db 298 GLKVISISNGGPTLF-OSNIGSSAGOGGGAINTIASAEELASISGSDITF-NNNOYVING 355

Qy 344 STDPKRAVNIIGNSGKFTFLRAKNHTIFPYDPTSGT--SSDVLKINNGSAGALNPY 401

Db 356 STST--RAINIIDTAKVTSIRAAATGOSIYYDPDINNGTASTDTLNLNADANSELEY 413

Qy 402 QGTLIFSGEITLADKLVAADNLKSSFTQPSVLSGGKLLQKGVTLSESTFSQEAAGSLIG 461

Db 414 GGAIVFSGEKLSPREKAIANVTSTIRQPAVLARGDVLRLRGVIVTFPDLTQSGSRILM 473

Qy 462 DSGTTLSTTASGITTNLGIIVDSLGKQPSVSLRAKGSANVIVSGKLNLDIGNIYES 521

Db 474 DGGTTLSSKENLISGLNLAVMISLDGTNKAALKEADKNISLSGTIALIDTGSFEYEN 533

Qy 522 HMFSDQAFSLKLTVDADVDTNVDISLIVPAEDPASEVFGQGVNVMNTTDTANNTK 581

Db 534 HNLKASATYPLLELTT-AGANGTITLGAISLTLLDPEPTHGYGVGNMOLSWA--NATSSK 590

Qy 582 EATAWTGTGVPSPERKSLVVCNTLMGVFTDIBSLQOLVEIGATGMEHKGGFVWSMTN 641

Db 591 IGSINWRTGTGPIPSERKSNLPLNSLMGCFIDIRSNQLNLETKSSQSEPFERELMLSGIAN 650
 Qy 642 FLAKTGDENRKGFPHRTSGGYVIGSAAH7PKDDLFTFAFCHLEPARDXOCFIANNHRTYGC 701
 Db 651 FFYRDSMPTFRHGFRHISGGYVALGIGATTPADBDQLTFAFCQLFARDNHILTKGHGDTYGA 710
 Qy 702 TLFFPHSHTL-QPOYVLLGLGAKFSESAIEKPREPLALDVQVSHSNGMETHYTSL 760
 Db 711 SLVPHHTEGLFDIANFL-WGKATRAPWVLSISQIIPLSFDKAFSLATDNHMKTYTDN 769
 Qy 761 PESEGSMEKCIAGIGIDLPEVLNSPHPLFTFTFIPOMVEYMYVQNSFFESSQGRGF 820
 Db 770 SIIRGSWRNDAPCADLGLSLPFVISVPY-LKVEVPFVQVYIYAAQODPYEYAEYBRAF 828
 Qy 821 SIGRLLNISIPVGAKEFVQDGDIGDSYTYDLSGFSVSDVYRNNPQSTATLVMSPDWKIRGC 880
 Db 829 NKSELINVEIPIGVTFEERDSKSEKGTYYDLTLWYIIDAYRRNPKCQSLIASDANMAAYGT 888
 Qy 881 NLKROAFLLRGSNNVYVNSNCELFGHYAMELRGSSRNHYVDVGTKRF 928
 Db 889 NLARQGSFVRANHPQVNPHEIFQGFAPFVRRSSRNHYTNLGSKPCF 936

RESULT 14
 H86492
 Pmp_3 [imported] - Chlamydia pneumoniae (strain J138)
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 09-Jul-2004
 C:Accession: H86492
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi-
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10873362
 A:Accession: H86492
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-772 <STD>
 A:Cross-references: UNIPROT:O9RB71; UNIPARC:UPI00000CC33; GB:BA000008; NID:G9876389; PIR
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: pmp_3_2

Query Match 33.3%; Score 1591; DB 2; Length 772;
 Best Local Similarity 42.7%; Pred. No. 6, 1e-82;
 Matches 337; Conservative 146; Mismatches 275; Indels 32; Gaps 14;

Qy 153 LVVAGNPESTADGGAKGASFLITGTSGDALFENNSSSTGCAIATAGARIANTGYVR 212
 Db 1 MLFSKNPFSTDGCAITAKTSLTGTMSGLFSENTSSKKGAIQTSDALITGNQGEVSF 60
 Qy 213 LSNIASTSGAIDDEGTSILNNKFLVF-----EGNAKTT-----GAIQNTASGSPEL 263
 Db 61 SDNNTSSDGAALFTEASVTTISNNAKVSFIDNKVTGASSTTGDMSGALCAVKTSTDTKV 120
 Qy 264 IISNNKTLIFASNVATSGAIIHAKKLASSGFTFELNNVSSAT-PRKGAISIDASGE 322
 Db 121 TLTGQMLFENNSTTGAIVYKKLDELASGLTIFSNNSVNGATAPKGAIAIDBSGE 180
 Qy 323 LLSLAETGNITFVRNLTTLTGSSTPKRNAINIGSNGKTELEPAAKHHTIFFYDPII--S 380
 Db 181 LLSLSDSGDIVFLGNTVLTST--TPGTNRSSIDLGTSAKRTALRSAAGRAIFYDPDPIITGS 238
 Qy 381 EGTSSDVAKINNKGASGALNPYCGTLFSGETLTADELKVADNKSAGFTOPVSLSGKLL 440
 Db 239 STYTVDVAKVETPPDSALQYTGNIIFTEGKLSFTFADSKNLTSLKLDQVTLISGGLSL 298
 Qy 441 QKGYTLLESTFSQEAAGSLGMDSGTTLSTTAGSIITNLGINVDSLGLQPVSLTAKGAS 500
 Db 299 KHGVTLQQAFTQQAQDSRLMDVGTTLE-PADTSTINNLVINISSIDAKKAKIETKATS 357
 Qy 501 NKVIVSGKLNLIDIEGNIVESHMFSDQLFSLKLITVDADVDTNVDISLIPVPAEDPNS 560
 Db 358 KNLTLISGTTLLDPGTGYENSHLRNPQSYDILIELASGTVS---TATTPPIIMGEKF 413


```

OY 561 EYEGOGQM -VNWTTDTATNTKEATATWTKTGFPSPEPRKALVONTLMGFTDIBLQ 619
Db 414 HYGOGTWGPFIWVGAST--ATFNWTKGYIPNPERGSLVBNLMAAFIDISLHY 470
OY 620 LVEIGATMEHKQGFVWSMTNFIHKTDENRKRKFRPHSGGYVIGSAAHFPKDLPFAF 679
Db 471 LMEIANEGLQDRAFCAGLSNFHHKOSTKTRRGFRHSGGYVIGNULHTCSIDLISAA 530
OY 680 CHLPARDKCFIAHNSRTYGTLFEKASHLQDONYLRLGRAVESALIEKPREIPLA 739
Db 531 QLFORDRDYFVAKNGOTVYGTLYYQHNET-----YSL-PCXLRCSLSYVTEIPVL 584
OY 740 LDVOVSFESHSDNRKETHYLSLPESBGSNSNCIAGIGLDPVLVSNBHPFKTFIQMK 799
Db 585 FSGNLSYHTHNDLTKYTTYPVKSGWGNDSFALFEGRAPICL-DESAFEEGYPMFMK 643
OY 800 VEMVYVNSNPSFESSDGRGFSIGRLNLSIPVGAKEF-VQGDIDBSYTYDLSGFSVDY 858
Db 644 LQFYAHQEGFEQCTEARFEGSSRLVNLAPITGIRPEKSDCODA-TYNTLTGITYDVLV 702
OY 859 RNNPOSTATLVMSPDMSKIRGANSROAFLLRGSNNVYNSNCELFHYAMELRGSSRNY 918
Db 703 RSNPDCTTLTASDGSWTKFGTNLARQALVLRAGNHCFPNSNFEAFSQFSFELRGSSRNY 762
OY 919 NVDVGTCLRF 928
Db 763 NVDIGAKYOF 772

```

```

Db      121 KTVTLGFSALSFLKSPASTVNTGLGAINVKGNLSLNDKXLIODNFSTGDGGAINCAG 180
Qy      172 FLATGSGDALFNNSSSSTGGALATTAGARIANNTRYVRFLSNIASTSGAIDDEGT91 231
Db      181 ----- 180
Qy      232 LSNKKEFLFEGNAKTTGGALCNTKASGPPELLISNNKTLIFASVVAETSGAIIHAKKIA 291
Db      181 ----- -SLKIANKSLSEGTGNSSSTRGGAIIHTKXLT 210
Qy      232 LSSGGEFFELKNNSSATPKGGAISIDASGELSLEFGNITFVAVNTLTTGSTGPBKN 351
Db      211 LSSGGETLFOGNTAPTAAGKGAIIADSGTISIGSGDIIIEGNTI-- -GATGVSHS 267
Qy      352 AINSGNKEFFELRAKXHTTFFYDPIITSEGRS-- -DVUKINGNSAGALNPYOGTILFSG 409
Db      268 AIDGTSKAITLRAGQHTTIFYDPIITVGTSTVADALANINSPDTGNKXETGTTIVFSG 327
Qy      410 ETLTDELKAVDNLTKESSFQPVSLSGGKLLQKGVTLTSTFSQENGSLLGMDSGTLLST 469
Db      328 EKLTAEAKDEKRNRSKULLQNVAFKNGIVLVKGDVVLANSNGSQDANSKLLINDLGTSLVA 387
Qy      470 TAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLANLIDIEGNIYESHMFSDOL 529
Db      368 NTESTIELNLNEINIDSLRNGKKIKLSATAQXDIRIDRPVVLAISDESFFQGLNEDHS 447
Qy      530 FSLKTIIVADADVDTNVDISLILPPAEDPNESEFFQCGMNWMTTDTNTNKEARATWT 588

```

RESULT 15
 E72130
 polymorphic membrane protein G family CP0761 [imported] - Chlamydomonas reinhardtii (strain 6802) [Chlamydomonas reinhardtii] (Chlamydomonas reinhardtii)
 C.Species: Chlamydomonas reinhardtii
 C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C.Accession: E72130 | G81541
 R.Katman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; ...
 Nature Genet. 21, 385-389, 1999
 A.Title: Comparative genomes of Chlamydomonas reinhardtii and C. trachomatis.
 A.Reference number: A72000; MUID:99206606; PMID:10192388
 A.Accession: E72130
 A.Molecule type: DNA
 A.Residues: 1-841 <REA>
 A.Cross-references: UNIPROT:Q9Z3A1; UNIPARC:UPI00000470B5; GB:AE001586; GB:AE001363; NID:
 A.Experimental source: strain CWM029
 R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A.Title: Genome sequences of Chlamydomonas reinhardtii and Chlamydomonas reinhardtii.
 A.Reference number: A81500; MUID:20150255; PMID:10684935
 A.Accession: G81541
 A.Molecule type: DNA
 A.Residues: 1-841 <REA>
 A.Cross-references: UNIPARC:UPI00000470B5; GB:AE002235; GB:AE002161; NID:g7189672; PIDN
 A.Experimental source: strain AR39, HL cells
 C.Genetics:
 A.Gene: pmp_2; CP0761
 C.Superfamily: Chlamydomonas reinhardtii polymorphic outer membrane protein G

Search completed: November 25, 2005, 14:21:16
Job time : 28.1039 secs

Query Match	30.0%	Score 1435.5	DB 2	Length 841
Best Local Similarity	35.9%	Pred. No. 46-73	Indels 125	Gaps 15
Matches	Conservative 147	Mismatches 335		
QY	1	MKTSIPWVIVSVSLAFS--CHLOSLNLEELSPDSFNGINDSGTEPTKPTSA---TTVSL	55	
Db	1	MKIPRLFILISVPLTSLMSNLLGAAATTEELASNSPDGTTSTPSKTSKTSATDGTNYVF	60	
QY	56	TDDVFPYE-PGKGTPISDCFKQ--TTDNUTPLNGHSLTEGFIDAGTHAGA-ASTTN	111	
Db	61	KDSVIAENVPKTGETOSTSCFNDDAAGLNLGGGFTFSFNIDATTAISGAISSEAN	120	
QY	112	KNLTFSGFLSLFSDSGPSTTVTTGGOTLSAGGVNLNRIKLVVANGFSTADGAIKGS	171	

QY 882 LSRQAFLLRGSNNYYNSNCELFGHYAMELRGSSRRYNYVDVGTKLRF 928

Db 795 LARQGIIVQASGFRSLGAAAEELFGNDFEWMGSSRRYNYVAGSKIRF 841

Search completed: November 25, 2005, 14:21:16
Job time : 28.1039 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 13:58:10 ; Search time 141.033 seconds
(without alignments) 4642.376 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 4782
Sequence: 1 MKTSIPWLVSSVLAFSCHL.....MELRGSSRNRYNDVGTKLRF 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4782	100.0	928	1	PMPL1_CHLPPN
2	1882	39.4	942	1	PMPL1_CHLPPN
3	1802	37.7	926	2	PMPL1_CHLPPN
4	1802	37.7	926	2	PMPL1_CHLPPN
5	1794	37.5	926	1	PMPL1_CHLPPN
6	1791	37.5	926	1	PMPL1_CHLPPN
7	1785	37.3	928	1	PMPL1_CHLPPN
8	1761	36.8	930	1	PMPL1_CHLPPN
9	1733	36.2	936	1	PMPL1_CHLPPN
10	1598	33.4	866	2	PMPL1_CHLPPN
11	1591	33.3	772	2	PMPL1_CHLPPN
12	1562.5	32.7	839	2	PMPL1_CHLPPN
13	1562.5	32.3	841	2	PMPL1_CHLPPN
14	1535	32.1	846	2	PMPL1_CHLPPN
15	1532.5	32.0	847	2	PMPL1_CHLPPN
16	1433.5	30.0	841	1	PMPL1_CHLPPN
17	1353	28.3	922	1	PMPL1_CHLPPN
18	1284.5	26.9	973	1	PMPL1_CHLPPN
19	1282	26.8	1024	2	PMPL1_CHLPPN
20	1275	26.7	1378	2	PMPL1_CHLPPN
21	1259.5	26.3	1011	2	PMPL1_CHLPPN
22	1237.5	25.9	843	2	PMPL1_CHLPPN
23	1222	25.6	700	2	PMPL1_CHLPPN
24	1205	25.2	840	2	PMPL1_CHLPPN
25	1203	25.1	1276	1	PMPL1_CHLPPN
26	1198	25.1	849	2	PMPL1_CHLPPN
27	1188	24.8	602	2	PMPL1_CHLPPN
28	1183.5	24.7	601	2	PMPL1_CHLPPN
29	1153.5	24.1	843	2	PMPL1_CHLPPN
30	1125.5	23.5	591	2	PMPL1_CHLPPN
31	1105.5	23.1	581	2	PMPL1_CHLPPN

Result 1	PMPL1_CHLPPN	STANDARD	PRT	928 AA
AC	086164	Q9K299		
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Probable outer membrane protein pmpl1 precursor (Polymorphic membrane protein 11) (Outer membrane protein 4)			
GN	Name=pmpl1; Synonyms=omp4; Ordered locus names=CP00449, CP0302, CPB0468;			
OS	Chlamydia pneumoniae (Chlamydia pneumoniae)			
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia			
OX	NCBI_TaxID=83558;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=CWL029/VR-1310;			
RX	MEDLINE=20007584; PubMed=9864239;			
RA	Knudsen K., Madsen A.S., Mygind P., Christensen G., Birkelund S.;			
RT	"Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae";			
RL	Infect. Immun. 67:375-383(1999).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=CWL029 / VR1310;			
RX	MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;			
RA	Kalman S., Mitchell W.P., Marathe R., Lamme C.J., Fan J., Hyman R.W.,			
RT	Olinger L., Grimwood J., Davis R.W., Stephens R.S.;			
RL	"Comparative genomes of Chlamydia pneumoniae and C. trachomatis"; Nat. Genet. 21:385-389(1999).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=CWL029;			
RX	MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RT	White O., Hickey E.K., Peterson J.D., Uettermann T.R., Berry K.J.,			
RL	Bass S., Linher K.D., Weidman J.F., Knout H.M., Craven B., Bowman C.,			
RA	Dodson R.J., Gwin M.L., Nelson W.C., Deboy R.T., Kolonay J.F.,			
RT	McCarty G., Salzberg S.L., Eisen J.A., Frazer C.W.;			
RL	"Genomic sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39";			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=AR39;			
RX	MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;			
RA	Medline=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;			

ALIGNMENTS

32	1102.5	23.1	1013	1	PMPL1_CHLPPN	086164	Chlamydia t
33	1040	21.7	987	1	PMPL1_CHLPPN	086164	Chlamydia m
34	987.5	20.7	868	2	PMPL1_CHLPPN	086164	Chlamydia m
35	851	17.8	878	2	PMPL1_CHLPPN	086164	Chlamydia m
36	849	17.8	878	2	PMPL1_CHLPPN	086164	Chlamydia m
37	846	17.7	878	2	PMPL1_CHLPPN	086164	Chlamydia m
38	843.5	17.6	878	2	PMPL1_CHLPPN	086164	Chlamydia m
39	837	17.5	878	2	PMPL1_CHLPPN	086164	Chlamydia m
40	837	17.5	878	2	PMPL1_CHLPPN	086164	Chlamydia m
41	836	17.5	878	2	PMPL1_CHLPPN	086164	Chlamydia m
42	836	17.5	878	2	PMPL1_CHLPPN	086164	Chlamydia m
43	835	17.5	878	2	PMPL1_CHLPPN	086164	Chlamydia m
44	833	17.4	878	2	PMPL1_CHLPPN	086164	Chlamydia m
45	831.5	17.4	427	2	PMPL1_CHLPPN	086164	Chlamydia m

RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CML029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RC STRAIN=TW-183;
 RA Geng M.M., Schumacher A., Muehlbauer I., Benesch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 RT other Chlamydia strains based on whole genome sequence analysis.";
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (potential).
 CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AJ001311, CA004672.1; -; Genomic DNA.
 CC EMBL, AJ133034, CAB37072.1; -; Genomic DNA.
 CC EMBL, AE001628, AAD18593.1; -; Genomic DNA.
 CC EMBL, AE002192, AAF38159.1; ALT INIT; Genomic DNA.
 CC EMBL, BA000008, BAA98658.1; -; Genomic DNA.
 CC EMBL, AE017158, AAP8399.1; -; Genomic DNA.
 CC PIR, D72077, D72077.
 CC PIR, H86546, H86546.
 CC PIR, H86546, H86546.
 CC PHCI-2DPAGE; O86164; -.
 CC TIGR, CP0302; -.
 CC InterPro: IPR005546; Auto_transpbeta.
 CC InterPro: IPR011427; ChlamPMP_M.
 CC InterPro: IPR003368; Chlamydia_PMP.
 CC Pfam: PF03797; Autotransporter; 1.
 CC Pfam: PF02415; Chlam_PMP; 6.
 CC Pfam: PF07548; ChlamPMP_M; 1.
 CC TIGRFAMs: TIGR01376; POMP_repeat; 5.
 CC Complete proteome: Membrane; Multigene family; Outer membrane; Signal.
 CC FT SIGNAL 1 24 Potential.
 CC CHAIN 25 928 Probable outer membrane protein pmp11.
 CC SQ SEQUENCE 928 AA; 98904 MM; 788BCDD62C911402 CRC64;
 CC -----
 CC Query March 100.0%; Score 4782; DB 1; Length 928;
 CC Best local similarity 100.0%; Pred. NO. 1.3e-256;
 CC Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 FTFLRAAKNHTTFPPYDPTSEGSSDVLKINNSAALNPYQGTILFSGETLTADBLKVA 420
 Db 361 FTFLRAAKNHTTFPPYDPTSEGSSDVLKINNSAALNPYQGTILFSGETLTADBLKVA 420
 QY 421 DNLKSFQPVSLSGGKLLQKGVTLKESMSFQSGASLGMDSGTLSTAGSIITNIG 480
 Db 421 DNLKSFQPVSLSGGKLLQKGVTLKESMSFQSGASLGMDSGTLSTAGSIITNIG 480
 QY 481 INVDSGLKQPVSLTAKGANKIVGSKNLIDIEGNIYESHMFSDQLFSLKITYDAD 540
 Db 481 INVDSGLKQPVSLTAKGANKIVGSKNLIDIEGNIYESHMFSDQLFSLKITYDAD 540
 QY 541 VDTNVDISGLIPVPAEDPNSEYFQCGQNNVNTTDTATNTKATATATWTKGFPSPBRKS 600
 Db 541 VDTNVDISGLIPVPAEDPNSEYFQCGQNNVNTTDTATNTKATATATWTKGFPSPBRKS 600
 QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFWSMTNPLAKTGDENRKGFRTSGG 660
 Db 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFWSMTNPLAKTGDENRKGFRTSGG 660
 QY 661 YVIGSAHTPKDULFTFAFCHLPARDKCFIAHNSRTYGTLPFGHSHTLQPNYLRIG 720
 Db 661 YVIGSAHTPKDULFTFAFCHLPARDKCFIAHNSRTYGTLPFGHSHTLQPNYLRIG 720
 QY 721 RAKFSBAIBKPREIPLADVVSFSHDNRMEHTYSLPESGWSNECIAIGIGLDL 780
 Db 721 RAKFSBAIBKPREIPLADVVSFSHDNRMEHTYSLPESGWSNECIAIGIGLDL 780
 QY 781 PFLVSNHPLFKFTIQMKEMVYVONSFEBSQGRGSIQRLNLSTPVAKFPVQGD 840
 Db 781 PFLVSNHPLFKFTIQMKEMVYVONSFEBSQGRGSIQRLNLSTPVAKFPVQGD 840
 QY 841 IGDSTYDLSGFVSDVYRNNPOSTATLVMSPSWKIRGSLRQAFLRGSNNVYNSN 900
 Db 841 IGDSTYDLSGFVSDVYRNNPOSTATLVMSPSWKIRGSLRQAFLRGSNNVYNSN 900
 QY 901 CELFGHYAMELRGSSRYNVDTGTLRF 928
 Db 901 CELFGHYAMELRGSSRYNVDTGTLRF 928
 Db 901 CELFGHYAMELRGSSRYNVDTGTLRF 928
 RESULT 2
 Q823X1.CHLCV PRELIMINARY; PRT; 942 AA.
 ID Q823X1.CHLCV PRELIMINARY; PRT; 942 AA.
 AC Q823X1;
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Polymorphic outer membrane protein G family protein/autotransporter,
 DE putative.
 GN OrderedLocustNames=CCA00282;
 OS Chlamydia caviae.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OC NCBI_TaxID=83357;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GRIC;
 RC MEDLINE=2256915; PubMed=12682364; DOI=10.1093/nar/31.21.3632;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
 RA Heidelberg J.F., Holtzapfel E.K., Knouri H.M., Fedorova N.B.,
 RA Carley H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J.,
 RA White O., Salzberg S.L., Heia R.-C., McClarty G., Rank R.G.,
 RA Bavoil P.M., Fraser C.M.;
 RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
 RT examining the role of niche-specific genes in the evolution of the
 RT Chlamydiaceae.";
 RL Nucleic Acids Res. 31:2134-2147(2003).
 DR EMBL; AE016395; AAP05033.1; -; Genomic DNA.
 DR TIGR; CCA00282; -;
 DR GO; GO:0019667; C:outer membrane; IEA.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR011427; ChlamPMP_M.
 DR InterPro; IPR003368; Chlamydia_PMP.


```
Dh 535 GGIGLSGKGSV-TTTNVSHVGVAE---THYGYQGMSVSWKDNNSDPKOTAIPTWN 590
Qy 589 KTGVPSPERKALVNCNTLWGVFTDIRSLQQLVEIGATG-MEHKQGFVWSMTNPLHKTG 647
Dh 591 KTGVPSPERARAPLVNLSLWGSFIDLRSLQDLERSVDSILETRGLWVGIGFFHKDR 650
Qy 648 D-ENRKGFRTSGGVIGSGAHTPKDILFTFAPCHLPARDKCFIAHNSRTYGGTLFPK 706
Dh 651 NAEHRK-FRHISGSGVIGATNTSREDLSVAFCQFAKDKDYLVSKNAANVAVGASYQQ 709
Qy 707 HSHTLQONVYRLGRKFSESAIEKFPREIPLADVQVSPSHSNRMETHYSLPESGS 766
Dh 710 HVSGFDDTLRFLNG---PNTCCSGFSKEIPIFLDAQITTYCHTANNMTTSTIDYPEVKG 765
Qy 767 WSNECIAGGIGLDLPF-VLSNPHPLFKTIPQMKVEMVYVQNSFFESSDGRGFSIGRL 825
Dh 766 WGNITLGLTLSTSPVPIPVFSS--SIFDSYAPFAKQVYVAHQDDPKETTEGRFESSDL 823
Qy 826 LNIISIPVGAKEVQGDIGDSTYYDLSGFVSDVYRNPNQSTATLVMSPDMSKIRGNSLRQ 885
Dh 824 LNVSVPIGIFKEKLSYGERSAVDLTLMYIPVYRHNPSCTGLAINDVSWLTATNLARQ 883
Qy 886 AFLRGSNVYVNSNCELFGHYAMELRGSSRNRYVDGTLRF 928
Dh 884 AFIVRAGNHIALTSGVEMFSQFGFELRSSRNRYVDLGAKVAF 926
```

RESULT 4

OSL6J3_CHLAB PRELIMINARY; PRT; 926 AA.

```
AC 05L6J3;
DT 01-FEB-2005 (TRENBLREL. 29, Created)
DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
DE Polymorphic outer membrane protein.
GN Name=pmp1G; Synonyms=pomp98A; OrderedLocuNames=CAB282;
OS Chlamydia abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=83555;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=526/3;
RX PubMed=15837807; DOI=10.1101/gr.3684805;
RA Thomson N.R., Yeates C., Bell K., Holden M.T.G., Bentley S.D.,
RA Livingston M., Cerdano-Tarraga A.-M., Harris B., Doggett J.,
RA Ormond D., Mungall K., Clarke K., Fellwell T., Hance Z., Sanders M.,
RA Quail M.A., Price C., Barrall B.G., Parkhill J., Longbottom D.;
RT "The Chlamydia abortus genome sequence reveals an array of
RT variable proteins that contribute to interspecies variation.";
RL Genome Res. 15:629-640 (2005).
DR EMBL; CR848038; CAH63732.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 926 AA; 98440 MW; F81C2A79A3D575D1 CRC64;
```

Query Match 37.7%; Score 1802; DB 2; Length 926;
Best Local Similarity 40.8%; Pred. No. 2.5e-91;
Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;

```
Qy 1 MKTSLPWLVSVLA--FSCHQLSLANELLSPDSPFNGNIDSGFTPKTATT-----YS 54
Dh 1 MKPSLYKLISLTLTIPISFHSQJHAHVALTQESILDAN--GAFSPQSTSTAGCTIYN 57
Qy 55 LTGVDFPEPGKGTPLSDSCFKQTTDNTLFLNGHSLTFGFLDAGTHAGAASTANRL 114
Dh 58 VESDLSIYDVQGTALASSAFVQTADNLTFLKGNHSLSTITANAGANAGINVTADKIL 117
Qy 115 TFSGSLSPDSSPTVYTTGGTSLSSAGVNLNIRKLVAGNFSADGAIKASFL 174
Dh 118 TLTDSKLSFKPCPSLVNTGKAMSGALNLANNAISLIFQNYSAENGALISCKASFL 177
Qy 175 TGTSGDALFSNNSSSTKGAITTTAGARIANNVGVPLSNASTSGAIDEGSILSN 234
Dh 178 TGSSKEISFTTNSYAKGALAAATGIAHLSDNGTIFRSGNTAVNSGAVVSEASMTIAG 237
```

```
Qy 235 NKELYEENAAKTT---GALICNTKASGSPELIISNNKTLIPASVASTSGAIIHAKU 290
Dh 238 NNVAVSNNAVSGSDGCCGALHCSKTGSAPLTIRDNKVLIFEENTSSAKGAIYTDKL 297
Qy 291 ALSSGFTPELRNNVSATPPKGAISIDAGELSLAEFGNITFVNTLTITGSDTTPPR 350
Dh 298 ILTSGPTAIKNNKVTAAHPKGAIGIAANGECSLAEHGDTIF-DNNLMATQDNATIKR 356
Qy 351 NAINISNGKFTELRAKNNHTIFFYDPTISEGSSDVLKINNSAGALNPYOGTILFSGS 410
Dh 357 NAINISNGKFTVLRPAASGKTIFFYDPTIEGNAADLTINKAEGD-KTYNRIILFSGE 414
Qy 411 TLTADELKVAADNKKSFQPSVLSGKLLIQKVTLESTFSQDAGSLGMDGTLTST 470
Dh 415 KLTQEOAAVADNKTFTQPTITLAAGELVRSGEVEAKTVQTAGSILLMDAGTKLSAK 474
Qy 471 AGSITITNLGINDSLQKQPVSLTKAGSNKIVYSGKNTLIDIBENIYESHMFSDQF 530
Dh 475 TEDATILNLAINTLIDGKKFAVVDAVAAGKNTLSGALGVLDPTGKFENHRLDNTLAL 534
Qy 531 SLKITVDADVDTNVDISLIPVPAEDPNSYQFGQGMVNMVTTDTATNTKEATA--TW 588
Dh 535 GGIGLSGKGSV-TTTNVSHVGVAE---THYGYQMSVSWKDNNSDPKOTAIPTWN 590
Qy 589 KTGVPSPERKALVNCNTLWGVFTDIRSLQQLVEIGATG-MEHKQGFVWSMTNPLHKTG 647
Dh 591 KTGVPSPERARAPLVNLSLWGSFIDLRSLQDLERSVDSILETRGLWVGIGFFHKDR 650
Qy 648 D-ENRKGFRTSGGVIGSGAHTPKDILFTFAPCHLPARDKCFIAHNSRTYGGTLFPK 706
Dh 651 NAEHRK-FRHISGSGVIGATNTSREDLSVAFCQFAKDKDYLVSKNAANVAVGASYQQ 709
Qy 707 HSHTLQONVYRLGRKFSESAIEKFPREIPLADVQVSPSHSNRMETHYSLPESGS 766
Dh 710 HVSGFDDTLRFLNG---PNTCCSGFSKEIPIFLDAQITTYCHTANNMTTSTIDYPEVKG 765
Qy 767 WSNECIAGGIGLDLPF-VLSNPHPLFKTIPQMKVEMVYVQNSFFESSDGRGFSIGRL 825
Dh 766 WGNITLGLTLSTSPVPIPVFSS--SIFDSYAPFAKQVYVAHQDDPKETTEGRFESSDL 823
Qy 826 LNIISIPVGAKEVQGDIGDSTYYDLSGFVSDVYRNPNQSTATLVMSPDMSKIRGNSLRQ 885
Dh 824 LNVSVPIGIFKEKLSYGERSAVDLTLMYIPVYRHNPSCTGLAINDVSWLTATNLARQ 883
Qy 886 AFLRGSNVYVNSNCELFGHYAMELRGSSRNRYVDGTLRF 928
Dh 884 AFIVRAGNHIALTSGVEMFSQFGFELRSSRNRYVDLGAKVAF 926
```

RESULT 5

PMP9_CHLNP STANDARD; PRT; 928 AA.

```
ID PMP9_CHLNP
AC Q92398;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable outer membrane protein pmp9 precursor [Polymorphic membrane protein 9] (Outer membrane protein 10).
GN Name=pmp9; Synonyms=omp10; OrderedLocuNames=Cpno447, CP0306, CPB0464;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CWI028 / VR3310.
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birke Lund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity";
RL Am. Heart J. 138:S491-S495 (1999).
RN [2]
```

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CWL029;
RX MEDLINE=9920606; PubMed=10192388; DOI=10.1038/7716;
RA Kaiman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,
RA Olinger L., Gitwood J., Davis R.W., Stephens R.S.,
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.",
RL Nat. Genet. 21:385-389(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AR39;
RX MEDLINE=2015025; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Lihner K.D., Weisman J.F., Khouri M., Craeven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.,
RT "Genome sequences of Chlamydia trachomatis Morn and Chlamydia
pneumoniae AR39.",
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CML029 from USA.",
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TW-183;
RA Gang M.W., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.",
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
(Potential).
CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC -1- SIMILARITY: Contains 1 autotransporter (TC 1.B.12) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AJ133034; CAB37069.1; -; Genomic DNA.
DR EMBL, AE001628; AAD18591.1; -; Genomic DNA.
DR EMBL, AE002192; AAF38163.1; -; Genomic DNA.
DR EMBL, BA000008; BAA98655.1; -; Genomic DNA.
DR EMBL, AE017158; AAP98395.1; -; Genomic DNA.
DR FPI, B72077; B72077.
DR PIR, E86546; E86546.
DR TIGR, CP0306; -.
DR InterPro: IPR005546; Auto transpheta.
DR InterPro: IPR006315; Autotransporter.
DR InterPro: IPR011427; ChlamPMP_M.
DR InterPro: IPR003368; Chlamydia_PMP.
DR InterPro: IPR006626; Pdh1.
DR Pfam: PF03797; Autotransporter_1.
DR Pfam: PF02415; Chlam PMP; 7.
DR Pfam: PF07548; ChlamPMP_M; 1.
DR SMART, SM00710; Pdh1; 5.
DR TIGRFAMs, TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs, TIGR01376; POMP_repeat; 6.
KM Complete proteome; Membrane; Multigene family; Outer membrane; Signal.
FT SIGNAL 1
FT CHAIN 26
FT SEQUENCE 27 928 Probable outer membrane protein pmp9.
SQ SEQUENCE 928 AA; 9633 MM; 58910A8F04F12219 CRC64;

Matches 404; Conservative 152; Mismatch 353; Indels 38; Gaps 17;
QY 1 MKTSIMVSVSYLAESCHLQ-----SLAEBLLSPDSFNGNDISGTFP-----KTSAT 51
Db 1 MSSLHMFLLSSLLPLSLNFSAPAAVEINLGFNFSG---PFTYPPPAQTNADET 57
QY 52 TYSLNGVFPFYEGRKTPIDSCFKQTDTNLFLNGHSLTGFIDAGTHAGAASTAN 111
Db 58 IYVLTDVGIITNAGSPITALTASCCKETGNLTFQGHGYQFLIONIDAGANC-TFTWTAN 116
QY 112 KULTFSGFLSDSPSTVTYTGCTLSSAGVNLNRLKLVNAGNESTAGALIKGAS 171
Db 117 KILSFSGFYSLS-1QTNATATGAIKSTACSTQSNVSCYFGQFNFDNGALQGS 174
QY 172 FLITGSGALFSSNNSSTKGAITTAGAIANNNGYRPLSNISTSGAIDDEGTSI 231
Db 175 ISLS-LNPULTRAKKATOKGALYSTGITTNTLNSFSFENTAAANGALYTASSF 233
QY 232 LSNKFLYFEGN---AAKTTGAI-CNTKASGSPILLISNNKTLIFASVAETSGAIIA 287
Db 234 ISNKAIISFINNSVMTSATGAIYCSTSAKPVLTLSDNGLNFIQTATISGAIYT 293
QY 288 KKLALSSGGFTPELRN-VSATPKGALISIDASGLISAETGNTTFYRNTLT-TGST 345
Db 294 DNLVLSGGPTTFKNNSAIDTAAPLGAIAIDSGSLISALGGDITFGNTVVKASS 353
QY 346 DPKRANINIG-SNGKFTELRAKNTTFEYDPIYPTSEGS--SDVYKINNGAGALNPYQ 402
Db 354 OTTRNSINIGNTAKIYQIRASQNTIIFYDPIITSTIALSDALNLNGPLDAGPAYQ 413
QY 403 GTILFSGETTLADELKVADNLKSPFQVSLSGKLLLOKGYLTLESTFSQEARGLIGND 462
Db 414 GIVFSGEKLEAEAEADNLKSTIQPQLTAGGQSLKSGVTLVAKSFSQSGSTLMD 473
QY 463 SGTTLSTGSGITITNLGINDSLGKQVSLTAKASKNVYSGCLNIDIEGNTYSEH 522
Db 474 AGTTLETAG-ITINNVLNVDSLKETKATLKAQASGVTLVSGSLVDPGNYEDEV 532
QY 523 MFSDQLFSLKLTVDADVDTNVDISLLPVAEDPNSYFGQGNVMTDTATNTKE 582
Db 533 SWNPQVFSCLTIT-ADPANIHTDLADPLEKPIHWGQGNALMSQEDTATKSA 590
QY 583 ATAATWTKTGVSPSEKSLAVCNLTLMGVTDIRSLQOLVEIGATGMEHKGFWSSMTNF 642
Db 591 ATLTWTKTYNPNBERGLVANTLWGSFVDRSILQVATKVRQSGEIRGICEISNF 650
QY 643 LKKTGDKNRKRRHTSGYVIGGSAHTPKDILTFPAFCHLPARDKCFIAHNNRYGGT 702
Db 651 FHKDSTKIKKGRPHISAGYVGAATTLTASDNLITTAFCOLFGKDRDHPINKRASAAYAAS 710
QY 703 LFFKSHHTLQPNVYLRBLGAKFSESAIEKFPREIPLALVOVSPFSHSDRMETHYSLPE 762
Db 711 LHLQHLATLSSPBLTY-LPGSES-----EQVLPDAQLSIYSKNTMKTYTQAPK 761
QY 763 SEGWSNECIAGIGLDLPFLVSNPHLPKTEIPQKMEVMYVVSQNSFPRESSD-GRGFS 821
Db 762 GESSWNNDCALIELASLPHTLASHGCLPHAFPIKXVASYIHQDSFEBRNTTVLRSD 821
QY 822 IGRLLNLSPVQAKPYQDIDGYSYTYDLSGFVSDVYRNNPOSTATVLSPPDSWKIRGN 861
Db 822 SGDLIVSVPIGITEFRFRNRERASYEATVIYVADYRKPNPCTTALLINTSMKTTGTN 861
QY 882 LSRQAFLLGSNNVYVNSNCELFQHYAMELRGSSRYNNVDYTKURF 928
Db 882 LSRQAGIGRAGIFVAFSPNLEVTSLNLSWEIRGSSRSRYNADLGKQKF 928
RESULT 6
ID 0823W9_CHLCV PRELIMINARY; PRT; 926 AA.
AC 0823W9;
DT 01-JUN-2003 (TRENDEL. 24, Last sequence update)

DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN OrderedlocusNames=CCA00284;
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GPIC;
RX MEDLINE=22561955; PubMed=12682364; DOI=10.1093/nar/gkh321;
RA Read T.D., Myers G.S.A., Brumham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,
RA Carcy H.A., Umayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
RA White O., Salzberg S.L., Heia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Fraser C.M.;
RT "Genome sequence of Chlamydia caviae (Chlamydia peitacti GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016995; AAP05035.1; -; Genomic_DNA.
DR TIGR; CCA00284; -; C:outer membrane, IEA.
DR GO; GO:0019867; C:outer membrane, IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto_transpcbeta.
DR InterPro; IPR011427; Chlammp M.
DR InterPro; IPR003368; Chlamydia_pmp.
DR InterPro; IPR006626; Pbh1.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF07548; Chlammp_M; 1.
DR Pfam; PF02415; Chlam_pmp; 6.
DR SMART; SM00710; Pbh1; 4.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; pomp_repeat; 5.
KW Complete proteome.
SQ SEQUENCE 926 AA; 98213 MW; 0E1062B0778658B2 CRC64;
Query Match 37.5%; Score 1791; DB 2; Length 926;
Best Local Similarity 40.5%; Pred. No. 1e-90;
Matches 382; Conservative 166; Mismatches 363; Indels 32; Gaps 16;
QY 1 MKTSPWLVSSVLA--FSCHLOSLANELLSPPDSFNGNIDSGTFPTKTA---TTPS 54
DB 1 MRPSLYKILISSTLIPISFPHSQVHAVALTOESVLDA--GAFSPQSTSTAGATTYN 57
QY 55 LTGVDFEPEPKGPRPLSDSCFKOTDNLTPFGNGSLTFPFIADGTHAGAASTANKL 114
DB 58 VESDISIVDAGGAAMVSAFAFVOTADDLTFKNGRSLAIENVNSGANFAGIYVSADKTL 117
QY 115 TFSGFLSPDSSPSTVTYTGQGLTSSAGVLENIKLVVAGNFSTADGAIKASFL 174
DB 118 TLTDSTLSPFKKCPHVTNTGKAVKSGGALNLANNASILFNQNHNSADGAIKASFL 177
QY 175 TGTSGDALFSNNSSTKGCALATTAGARIANNNTGYRRLSNASTSGAIDEGTSLISN 234
DB 178 TGSSKEISFTTNTSTYKGCALATGAVANLSDQGVIFSGTAVANSAGVAEAENTTTAG 237
QY 235 NKFLYEEGNAKKT---GGAICNTKASGPELIISSNKTLLIPASNVETSGGAIIHAKL 290
DB 238 NSAVFNNNAVTGTTDGGCGGALHCKGTATPVLTIRKDKVLLFKENTSAAGAIYADKL 297
QY 291 ALSGFEFLNANNYSATPKGSAISDASGELISAETGNTTFVRNTLTGSGTDPK 350
DB 298 YLTSGGPIVFGONKATNAAPKGAIGIANGECSTIAHGDTTF--ENNLINATNATYKR 356
QY 351 NAININGSGKFTLPAANKHTTFPYDPITSEGTSSDVLLKINNGSAGALNPYQGITLFSGE 410
DB 357 NAINIEGNGKFEVNLRAASGNTLTFYDPVIGGTADLLTN--QAEGTKVNGRIIFSGE 414
QY 411 TLTADELKVAADLKSSFTQPSVLSGGKLLQKGVLTLESTSPSGEGLLQMDSGTTLST 470
DB 415 KLTEDOTADADNLKTVFTOPIALAAGEELLRNGVEVEAKVASQTAGSLILIDAGTKLSAK 474

QY 471 AGSITTTNIGINVDLS-GLKQPVSLTAKGASNKVYSGKLNLIIDEGNITYESHMFHDOL 529
DB 475 TEDVTILTNLAIPNNSLDGTFKIAVIAVANAKN-VVTGAIIGIIDPGKFEEDKLNETLA 533
QY 530 FSLKITTVDADVNTNDISLIVPADDPNSEIGFGGONNVMTTPTATNTEATA--TW 587
DB 534 LGGIQFSAKGSI-TTIDVBP--TTTRSPAQHGYGQNSLSWITNGSDPKQTAVFNM 589
QY 588 TKTGFPSPERKSALVNTLMGVFTDIRSLQOLVEICA-TGMEHKQGFVWSMTNPLAK- 645
DB 590 NKGYNPNRPARAPVLVNSLMSGFMDIRSLQDMESVDTLLETTRGLVWSGNGNLHMD 649
QY 646 TGDENRKGRFHNSGGYVIGGSAHTPPKDLFTFAFCHLPADKDCFLAHNNSRTYGTLPF 705
DB 650 PSANENK-FRHISSGGYLGATNTTQEDTLISVAFCOLFGDKXLYLAKNAANYAASIIYY 708
QY 706 KHSHTLPQNYLLGSAKSESALIEKPPREIPLALVOVVSFHSNDRMETHYSLFESSG 765
DB 709 QHVSKEPDLTRLFNG---PNTCCSGFSKEIPLFLDAQVYCHTNMTTYYDYDEVKG 764
QY 766 SMNECIAGIGLDLPVLSPNPPLPKTFIPQKVMVYVVSQNSPFESSSDGRGFSIGRL 825
DB 765 SKGNDVYVALSTSVPIPIPT-HAFDVSAPFAKLQVYVAHQDFEPTREGTFESSDL 823
QY 826 LNSIPVGAKEVQGDIGDSTYTLDSGFVSDVYRNNPOSTATILVMSPSDKIRGNSLRQ 885
DB 824 LNVSPIGVFEKLVGGEKTAVDLTLMVYDVYRHNPCITGPAINDVMTLTATNLARQ 883
QY 886 AFLRGSNNVYVNSCELFGHYAMELRGSSRRNVNVGKLRP 928
DB 884 AFLIRGNHLIAVTSGFEMFSQFGFELRSSRRNVVDLAKAVSF 926
RESULT 7
PMP10_CHLPN
ID PMP10_CHLPN STANDARD; PRT; 928 AA.
AC Q9RB65; O86163; Q9RB64; Q9S6P2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Probable outer membrane protein pmp10 precursor (Polymorphic membrane
DE protein 10) (Outer membrane protein 5).
GN Name=pmp10; Synonyms=omp5; OrderedlocusNames=CP0303, CPB0467;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CWL029 / VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk B., Birkeind S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J.,
RA Baas S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwin M.L., Nelson W.C., Deboy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Moyn and Chlamydia
RT pneumoniae A39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=uj138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi T., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kunara S., Nakazawa T.;

RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TW-183;
RA Geng M.W., Schumacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marx R., Meichers K.,
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis."
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1-914.
RC STRAIN=CML029/VR-1310;
RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christensen G., Birkelund S.,
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
RT membrane proteins of Chlamydia pneumoniae."
RL Infect. Immun. 67:375-383(1999).
CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies
CC (potential)).
CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ133034; CAB37071.1; -; Genomic DNA.
DR EMBL; AE002192; AAF38160.1; -; Genomic DNA.
DR EMBL; BA000008; BAA98657.1; -; Genomic DNA.
DR EMBL; AE017158; AAP98398.1; -; Genomic DNA.
DR EMBL; AJ001311; CA04671.1; -; Genomic DNA.
DR PIR; G81591; G81591.
DR PIR; G86546; G86546.
DR PHCI -2DPAGE; O86163; -.
DR TIGR; CP0303; -.
DR InterPro; IPR005546; Auto_transp_beta.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR011427; ChlamPMP.
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR006626; PBH1.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlam PMP; 7.
DR Pfam; PF02548; ChlamPMP_M; 1.
DR SMART; SM00710; PBH1; 4.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 5.
KM Membrane; Multigene family; Outer membrane; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 1 25 Probable outer membrane protein pmp10.
FT CONFLICT 305 305 Missing (in Ref. 4).
SQ SEQUENCE 928 AA; 97230 MW; 0590D5206A1DD0E1 CRC64;
Query Match 37.3%; Score 1785; DB 1; Length 928;
Best Local Similarity 40.4%; Pred. No. 2.2e-90;
Matches 385; Conservative 173; Mismatches 344; Indels 52; Gaps 18;
QY 1 MKTSIPVAVSSVLA--FSCHLQSLANEELSPDPSFNGNIDGTFPTPKTSAT--TYSLT 56
DB 1 MKSQPSMLVSLSTLACTSCSTVFAVAENIGPDSFSDGNTNCTYTPKNTTGIDYTLT 60
QY 57 GDVFFYEPKCKTPLSDSCFCQKTDNLTFLNGSHLTGCFIDAGHGAASLTANKLTF 116
DB 61 GDITLQNLGSAALTKCGFSDDTESLSFPAKGYSLSPLNTKSSAE--GAALSVTTDKLSTL 119
QY 117 SGFSLSPDSSPTVT--GQGTLSAGGVNLENIRLVVAGNFTADGATKAGASFL 174
DB 120 TGRBSLFLAAPSIVITTPSGKGVKCGDLTPTNNNTIIFKQDYCENGALSTKLSL 179
QY 175 TGRSGDALFSNNSST--KGAIAATTAGARIANNNGVYVFLSNIASTSGAIDECTST 231

DB 180 KNSTGISFEGNKSATGKKGAIICATGTVDTNNAPTFLFSNNIAEAGAINSTGNC 239
QY 232 LSNKKFLYEGNAKTT---GGAICNTKASGSPELIISNNKTLIFASNAVETSGAIIAK 288
DB 240 ITGNTLVFSNSVTTAAGGAL---SGDAVITSGNSVTSFGNVAANGAIIYAK 294
QY 289 KALSS--GGFTFLNNVSSATP--KGAISIDASGELSIAETGNITFVRNTLTGTS 345
DB 295 KLTLAGGGGGISFSNNIVOGTTAGNGAISTILAAGECSLSABAAGDITFGNAIVAT--TP 353
QY 346 DTFKRAINIGSKRTFLRAKNHTIFFYDPTIS--GTSNVKLKNGSAGALPQY 403
DB 354 QTTKRNSTIGSTAKTTLNRAISGHSIFFYDPTTANTAADSTDTLNLAKADAQNSTDYG 413
QY 404 TILFSEGTITADELKYADNLKSFPTQVPSLGGKLLQGVTLSETSFSGEASLLGMD 463
DB 414 SLVFSSEKLSDEDAKADNLSTLKQPVTLTLAGNLVKKGVLLDTGFTQTAGSSVYMDA 473
QY 464 GTTLSTTAASTITTNIGINVDLSGLNQPVSITAKGASNKVIVSGKMLIDIEGNIYESHM 523
DB 474 GTTLKASTEBVTLTGLSTIPVDSLGEKKVVIASAASKNVALSGPILLDQNGAYENHD 533
QY 524 FSHDQFLSLKLTVDADVDTNDISLIPVPAEDPSEYFGQGMVNMWTTDTAT--NRK 561
DB 534 LKGTQDFSFVQLSA--LGTATTTDVA---VPTVATPTHGYOGTWMGTWVDASTPKTK 569
QY 582 EATATWTKTGFPSPERKSAIVCNLTLMGVFTDIRSQQLVEIGATGMEHKQGFWSMTY 641
DB 590 TATLAWNTGYLNPFRQGLVFNLSMGFSBDIQAIGVIESALTLCSDRGMVAAGVAN 649
QY 642 FLAKTGDENRKGFRHTSGGVVIGSARTPKDDLTFPAFCHLPARDKCEIAHNSRTYGG 701
DB 650 FLQDKKGEKRRKRRHSGGVAIGAAQTCSENLISPAFQLGSDXDFLAKKHTDTYAG 709
QY 702 TLFFKASHTLQPNYTLRLGAKFSESAIEKP---REIPLADVQVSHSHDNMTHTYT 758
DB 710 AFYIQHITEC-----SGFTIGCLDKLPQSGSMHKLPLVEGQIAYSHVSDLTXYT 759
QY 759 SLPESSGWSNNECIAGIGLDLPVLSNPH---LKFPTIPQMKVEMYVVSNSPFEES 814
DB 760 AYPEVKSGWGNNAFNMMLGAS---SHSYPEVLCFTDYAPYIKNLTYIRDSSEKG 814
QY 815 SDGRGFSIGRLNLTSLPVGAKFVQGDIGSYTYDLSGFSVDYRNNPOSTATLVMSPPS 874
DB 815 TEGRSFDDNLTFLSLPIGVKEFKESDCNDFSDLTLSVPLDIRNDPCTTALVLSGAS 874
QY 875 WKIRGNLSRQAFLEFGSNVYVNSNCELFGHYAMELRGSSRYNVVDVTKLRE 928
DB 875 WETVANNLAROALQVAGSHYAFSPWFVEVLGQFVEFRVSSRIYVNDLGKRFQF 928
RESULT 8
PMP8_CHLPN STANDARD; PRT; 930 AA.
AC Q9J393; Q9RB66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
DE protein 8) (Outer membrane protein 11).
GN Name=pmp8; Synonyms=omp11; Ordered locus Names=CP00446, CP0307, CPB0463;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.
OX NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CML029 / VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christensen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.,
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity."
RL Am. Heart J. 138:S491-S495(1999).

RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;
 RA Kaitman S., Mitchell W.P., Marathe R., Lamell C.J., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
 RA Read T.D., Burnham R.C., Shen C., Gili S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J.D., Uetebach T.R., Berry K.J.,
 RA Bass S., Linkey K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
 RA Dodson R.J., Gwin M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
 RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mohn and Chlamydia
 pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.6.1397;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=TW-183;
 RA Geng M.M., Schumacher A., Muehlbauer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 other Chlamydia strains based on whole genome sequence analysis.";
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
 CC -1 SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 (potential).
 CC -1 SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC -1 SIMILARITY: Contains 1 autotransporter (TC 1.B.12) domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC
 CC EMBL; AJ13034; CAB37068.1; -; Genomic DNA.
 CC EMBL; AE001627; AAD18590.1; -; Genomic DNA.
 CC EMBL; AE002193; AAF38164.1; -; Genomic DNA.
 CC EMBL; BA000008; BAA98654.1; -; Genomic DNA.
 CC EMBL; AE017158; AAP98394.1; -; Genomic DNA.
 CC PIR; A81591; A81591.
 CC PIR; D72078; D72078.
 CC PHCI-2DPAGE; Q92393; -.
 CC TIGR; CP0307; -.
 CC InterPro; IPR005546; Auto_transbeta.
 CC InterPro; IPR006315; Autotransporter.
 CC InterPro; IPR01427; ChlamMP_M.
 CC InterPro; IPR003368; Chlamydia_PMP.
 CC Pfam; PF03797; Autotransporter; 1.
 CC Pfam; PF02415; Chlam_PMP; 6.
 CC Pfam; PF07548; ChlamMP_M; 1.
 CC TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 CC TIGRFAMs; TIGR01376; PMP_repeat; 6.
 CC Complete proteome; Membrane; Multigene family; Outer membrane; signal.
 CC SIGNAL
 FT CHAIN 1 26
 FT VARIANT 177 930
 FT 177 177
 FT
 FT SEQUENCE 930 AA; 97670 MW; 46A9B5E3BB913C4C CRC64;

Query Match 36.8%; Score 1761; DB 1; Length 930;
 Best Local Similarity 41.7%; Pred. No. 4,7e-89;
 Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;
 QY 1 MKTSIRWVVSSTLASCLOSAN---BELSPDSEFNQINDSGTFPEKTA---TTY 53
 DB 1 MKTPIHKLKLISSLTVPPI-LTSIATYGADASJSPDSEFG-AGGTFPEKSTADANGTY 58
 QY 54 SLTGDFVFEYEPGKGTPLSDSCFCQTTDNLTLFGNGHSLTFEGIDAGTHAGAASTYANKN 113
 DB 59 VLSGNYIINDAGCGTALTGCCFTETTGDLTLFGKGYSPFNVDAGSNAGAASTYADKA 118
 QY 114 LTFSGFSLSPDSEPTTYTTGGCTLSAGGVNLENIRKLVAAQNSTA---DGAIKKA 170
 DB 119 LFTFGFSNLSFIAPGTVAAGKSTLSAGANLTDNGTILFSQVNSNANNNGAIITTK 178
 QY 171 SFLTGTSQDALFNNSSSTKGAIATTTGARIANNQYVRFPSNASTSGAIDDEGTS 230
 DB 179 TLSISGNTSSITFTSNAKKLGGALYSAAASISGNTGQVFNANNKGETGGALGFAS 238
 QY 231 ILSNKKFLYFEGNAAKTT---GGAICNTFASGSPFLIISNNKTLFASVNAETSGAIIHA 287
 DB 239 SITQNSLFPSSGNTATDAAGKGAICYCKTGTPTLISGNKSLTFABNSVTYGGALICA 298
 QY 288 KKLALSSGGTFELRNNV-SSATPKGGAISIDAGSLISAETGNTTPVRYNTLTGGSTD 346
 DB 299 HGDLISAAGPTLFSNNRCGNTAAGKGAIAIDSGSLSSANQGDITFTGNTLTST-SSP 357
 QY 347 TPKRNALINGSNCKFELBAAKNHTIFPYDPTISSET-SSDYKINNGSAGALNPPYQNT 405
 DB 358 TSTRNALIYSSAKITNLRAAGOSIYFDPLASNTTSGASDVLTINQPPNSLDTYSGTII 417
 QY 406 LFGSETLTADDELTVADNLKSSFTQPVYLSGGKLLLOKGYLTBESTSPQOAGSLIGMDSGT 465
 DB 418 VFSGEKLSADEAQAANFNSILKQPLASGTLALGNVELDVNGRTQREGSLTLNQPGT 477
 QY 466 TLSTAGSTITNVLGNVDSGLKQVPSLTAKASKNVYSGKLNLDIEGNITESHMFS 525
 DB 478 KLADTDEALISLTKLVNLSLBENKSVSIETAAANTITLTSLPVDQSDSGNFESHTT- 536
 QY 526 HDQLFSL-LKITVDADVNTVDISLIPVPAEDPNSEYGGQGMVNTTDTATNKAT 584
 DB 537 -NOAFQPLVFTAAATASDIYIDALTSVQTPPEPHYIGQGWKATW-ADIST-AKSGT 593
 QY 585 AATYKTGFVSPSRKALVQNTLGVFTDIRSQQLVEIGATGMEHKQGFVWSMTNPLH 644
 DB 594 MTWTTGYNPNPERRASVVPDSLMASFTDIRTLQQLMTSQANSIYQQRGLMAGTANFTH 653
 QY 645 KTGDENKGRHTSGGYVIGGSAHTPKDGLFTPAFCHLPARDKOCFLAHNSRTYGGTLF 704
 DB 654 KDKSGTQAFRRHKSYGIVYVGGSAEDSESENFVAFCOLFGKDXDLFIVENTSHNYLASLY 713
 QY 705 FKSHTLQPNVYLRGAKFSESAIEKPREIFLALDVQVSPFSHSDNBMETHYTSPESE 764
 DB 714 LQHRALFG-----GLPMPSPGSIYDMLKDPLILAAQLSYSTYKNDMDRTYTSPEAQ 766
 QY 765 GSMSNECTIAGCIGLDLPFVLNSNPHLPKFTFIPOMKVMVYVSQNSPFESSSDRGFSIGR 824
 DB 767 GSWTNNSGALELGGSLALVLPKPAFPQGYFPLKQAVYSRQNFESGABARAFDGD 826
 QY 825 LNLISIVPAKPVQGDIGDSYTYDLSGFVSDYVRNNPOSTATLVNSPDWKIRGGLSR 884
 DB 827 LVNCSIPVGIARLEKISDEKKNFEISLAIYIGDVAKKPSRSTLWVSGASWTSLSCKNLAR 886
 QY 885 QAPLIRGSNNVYVNSNCELFGHYAMELRGSSRNRYNDVQKLPF 928
 DB 887 QAFLASAGSHLTLSPHEVLSGEAYELRGSAAHYINVDGRLYSP 930
 RESULT 9
 PMP7_CHLPPN STANDARD; PRT; 936 AA.
 ID_PMP7_CHLPPN
 AC Q92898; Q9J542; Q9J504;

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update) [Polymorphic membrane
DE Probable outer membrane protein pmp7 precursor (Polymorphic membrane
DE protein 7) (Outer membrane protein 12).
OS Name=pmp7; Synonyms=omp12; Orderedlocustnames=CPN0445, CPB0462;
GN Chlamydia pneumoniae (Chlamydia pneumoniae)
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomphila.
OX NCBI_TaxId=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CWL029;
RC MEDLINE=99206606; PubMed=101923388; DOI=10.1038/7716;
RA Kaiman S., Mitchell W.P., Marathe R., Lemmel C.J., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AR39;
RC MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.F., Uetachak T.R., Berry K.J.,
RA Baas S., Linher K.D., Weidman J.F., Khouri H.M., Craen B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.W.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=J138;
RC MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shira M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TW-183;
RC MEDLINE=TW-183;
RA Geng M.M., Schuhmacher A., Muehlhofer I., Benesch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Bessig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE OF 658-936.
RC STRAIN=CWL029 / VR1310;
RC MEDLINE=20007584; PubMed=10539856;
RA Christensen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkeund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
RN [6]
RP SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
CC (Potential).
CC -I- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC -I- SIMILARITY: Contains 1 autotransporter (TC 1.B.12) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AE001627; AAD18589.1; -; Genomic DNA.
CC EMBL; AE002193; AAF38165.1; -; Genomic DNA.
CC EMBL; BA000008; BAA38653.1; -; Genomic DNA.
CC EMBL; AE017158; AAP98393.1; -; Genomic DNA.
CC EMBL; AJ133034; CAB37067.1; -; Genomic DNA.
CC PIR; B81591; B81591.
CC PIR; C72078; C72078.

Query	Match	Similarity	Score	DB 1	Length	Gaps		
Query	Best Local Similarity	36.2%	Score 1733;	DB 1;	Length 936;			
Matches	378;	Conservative	182;	Mismatch	356;	Indels 32; Gaps		
DB	1	MKTSIPMWLVSSVLAFC	SCHLQSLANEELSPDSDFNINISDGF	-----	TPKTSATYTS	55		
DB	1	MKSSVSMVLFSSRI	LFSSLSIVAAEVLDDSSNNYS	DS-NQTTTVBPTDAAAGT	YSL	59		
DB	56	TGDFVFEYEPK	-GTPILSDSCFKQTTDNL	TELGNGHSLTFGEIDAGHAGAA	ASTT-ANKN	113		
DB	60	LSDVSPQNALG	PIPLASGCFLEAGD	ULFGQNHALKFARINAGSSAG	VASTADKN	119		
DB	114	LTFSEGFSLSPDSSP	STTVT-TGGCTISAGAGVNL	ENIRKLVAGNPS	STADGAKGASF	172		
DB	120	LLFPNDFPRLSI	ICPSLILSPGQCALKSVNLS	LTGNSQIIFQNPSSD	GVINTNF	179		
DB	173	LLATGSDALF	PNSSNSST--KGAIAITTAGAR	INNTGYVFLFNINISTG	SGALIDEGTS	230		
DB	180	LLSGTSPAFS	SRQAFATGKQGGVVA	TGTTTINSFGIYSF	SONLAKGSGGAL	YSTDNC 239		
DB	231	ILSNKFLYE	EGN---AAKTGGAICNT	YASGSPELIISNNKTL	IFASVAETSGA	IIH 286		
DB	240	SITNPQV	IPDGNASAMEAQOG	ALICTTTDK--VLTGNK	LSFTNNALYGA	IS 297		
DB	287	AKKIALSSGG	TEFLRNNVSSATP--KGAIS	IDASGEISLSAETG	NIITVRKTLTTG	343		
DB	298	GLKVISIAGG	PTLE-QSNISSGSSAGCGG	GAININIASGELL	SATSGDITF-NNNQV	TNG 355		
DB	344	STDPKRNAIN	ISNGKFTBELRAKNHT	IPYDPTSEGT--SSD	YV	KINGSGALNPY 401		
DB	356	STST--SNAIN	IIDTAVTISRATGOS	IIFYDPTNPGTAS	TDTLNLNADANSE	IEY 413		
DB	402	QGTLLFSGE	TLTADELKVADNLK	SSFPQVSLSGAKLL	LQKVTLEST	FSQEAGSLIGM 461		
DB	414	GGAIVFSGE	KLSPREKAIANVTST	IQPRAVLANGD	LVLRGVVPT	PKDLTQSGSRILM 473		
DB	462	DSGTTLST	AGSITITNMG	INVDLSGLKQPVSL	TAKAASKNVIVS	GKLNILIDICNIYES 521		
DB	474	DGGTTL	LSAKEANISL	INGLAVNLSL	IDGTNRKALTE	ADAKNISLSGTALIDT	SGSFYEN 533	
DB	522	HMFHDL	FLSLKLTVDADVD	TNDISLLFVPAED	PNSEKFGQGMVNM	TTDTATNTX 581		
DB	534	HNLSAST	PTLELT--AGANGT	ITLALSTLLQEP	PTHGVOGNQ	LSAA--NAVSSK 590		
DB	582	EATATMTK	GTGVPSPERK	SLVCTMLGV	FDIRSLQOLV	EIGATGMEHKG	GFVWSTMN 641	
DB	591	IGSINM	RTGVTIPPERK	SNPLNSLWGN	PLDISINQ	LITKSSGDFE	BEELWLSGIAN 650	
DB	642	FLHKTDEN	RKGFRHTSG	YIVIGSSAHT	PKXDLFT	PAFCHLFAADK	CFIAHNSRTYGG 701	
DB	651	FFYDSDM	PTBTRGHGF	NIISGVALGIT	TATTPAED	QLTFAFCQIFAD	RNRHNTIGKN	GDYGA 710
DB	702	TLFPKSH	HTL-QPNYV	ILGRAKS	ESAEKFP	REITPLAD	VDVQSF	SHSDRMETHYSL 760

Db 711 SLVFHHTGFLDIANFL-WGKATRAPVWLSEISQIILPSFDAKRSYLHTDNHMKYTTDN 769
Qy 761 PSESGWSNECIAAGIGLDLPFVLSNPHLPKFTPIPMKEMVYVSSONSFFESSDGRGF 820
Db 770 SITKGSNRDAFCADLGAASLPVIVSVRY-LLKEVEPVVKQYIYAHQODYEKAEGRAF 828
Qy 821 SIGRLNLISIPVGAKEVQGDIGDSYTYDLSGFFVSDVYRNNPOSTATLVNSPDSWKIRGG 880
Db 829 NKSLEINVEIPDIGVTFERDSKSEKGYDTLTLMYLILDAYRRNPKQOTSILASDANMAYGT 888
Qy 881 NLBROAFLRGSNVYVNSNCELFHGYAMELRGSSRNRYVDGTRKLF 928
Db 889 NLARQGSVRBAANHFOVNPHEIIFGQFAFEVRSSRNNTLGSKECF 936
RESULT 10
0823X0_CHLVCV
ID 0823X0_CHLVCV PRELIMINARY; PRT; 866 AA.
AC 0823X0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN OederedLocustNames=CCA00283;
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=83557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,
Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J.,
Bavoli P.M., Fraser C.M.,
RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AB016995; AAP05034.1; -; Genomic_DNA.
DR TIGR; CCA00283; -
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto.transbeta.
DR InterPro; IPR011427; ChlamPMP_M.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; ChlamPMP_M; 1.
DR Pfam; PF02415; ChlamPMP_M; 5.
DR TIGRFAMs; TIGR01414; autotrans bar1; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 4.
KM Complete proteome.
SQ SEQUENCE 866 AA; 92969 MW; 6CFAl4937C69DB30 CRC64;
Query Match 33.4%; Score 1598; DB 2; Length 866;
Best Local Similarity 37.5%; Pred. No. 4.6e-80;
Matches 357; Conservative 169; Mismatches 316; Indels 110; Gaps 21;
Qy 1 MKTISIPWLVSSVLAFCSHLO-SLANEELSPDDSFNGNIDSGFTPK--TSATYSLTG 57
Db 1 MKHPVYVWLVSSGLASTSLSPAFAVQETLNSDSYNNAATTDFAQTETTTGALEYTCG 60
Qy 58 DVFEPEPKGTPPLSDSCFKOTDNLTFINGHSLTFGFGIDACTAGAAASTTAKNLTFS 117
Db 61 NVCTTYAKTPTPLTKSCFTEETENLTFIGGYSLCFDNITVAKPAALVEVAADKTLSIS 120
Qy 118 GFSILSPSSPSTTYTTTGTGTLSSAGVNLKIRLVVAGNFSFADGAIKAGASFLTLTG 177
Db 121 GFSILSPSCYCPBG--TTGGAIKSGGTATFPDNNSTLTKSKNCSSEGAIAINCKSLTLKNS 178
Qy 178 SGDALFSNNSSSTKGAIATTAGARIANNVGRFLSNIASTSGAIDDEGTSILSNKF 237

Db 179 SVCANFIKNSDKKGAI----- 196
Qy 238 LVEGNAAKTGGATCNTRKASGPELISNNKTLIPASVVAETSGAIAHAKKLALSGGCF 297
Db 197 -----YCSDE-----NQLENNQMLFSEHTSBEBAIYAKKLALISISGCP 237
Qy 298 TEFLRNVS-SATPKGAISI-DASGELSLAETGNITVRNTLTGTSOTPKRNALNI 355
Db 238 TLFSSNSTSKADPKGAIICIAADSECSLTLENGIIPDGKIIITGGPST-KRNSIDL 296
Qy 356 GSNKRTFLRAKNHIFPYDPITTSRGTSSDYLIKINNSAGALNPQGTILFSGETLTAD 415
Db 297 GSGKFSQLRARDGFCVFPFYDPIANNNGSDTLEIKADGAA--TYSGLVFSGEKLTID 354
Qy 416 ELKVADNLKSSFTOPVLSGKLLQKGYLTLESTSPQSGSLGMDSGTTLSTTGA 475
Db 355 EKQVTDNLKLSFFQPIPLTVSSGSLVKNQVTSKQITQSGGA-IEMDAGTNTLTSTEDIS 413
Qy 476 ITNLGINVDSL--GLQPVSLTAKGASKVIVSGKLLIDIEGNIESHMFMSHQLF-S 531
Db 414 LSNLVINTSLGGGVPPLAAQISABG-TKNSVTISSLNVADGNGYEVPVSTSTREFPS 472
Qy 532 LKITYDADVDVNTVDSILIPVAEDPNESEYGGOGOMVNTTDTATNKRATATWTKG 591
Db 473 IIEAKANGTGTPTIPTHLTD--HAPAAHYGQGLMTTSMQGTATTSQATLAMAQQTG 529
Qy 592 FVPSPERKSLVNTLMTGVTDIRSLQQLVEIGATGMEHKQGFVYSSMTNPLHKTGBNR 651
Db 530 YNPNPERQGLVNTLMGSPSDVRAIQLNMDISVNADYQRGIMAGLANFLQKSGTERK 589
Qy 652 KGFRTSGGVYIGGSAHTPKDLPFAFCHLPARDKOCITLAHNSSTYGGTLFPKSHLT 711
Db 590 RKRRHNSAGVIGVAKYKTLSDVFSAAFCOLFPDRDXYLVSKNSNIYVGSIIYHGF 649
Qy 712 QPNYV---RLGAKRSBSAIEKPREIPALDVOYFSFSDBRMTHTS-----L 760
Db 650 DAVDNLQSTLG-----AQPVLVLAQULTRHSHSDMTKTTTKAAPQGVY 696
Qy 761 PSESGWSNECIAAGIGLDLPFVLSNPH-PLKFTPIPMKEMVYVSSONSFFES-SSDGR 818
Db 697 PELKGMQNDPCFVELGATVP--IESPYSLLFMYSPPLRFQVLVVAHQEDFKENNSTEGR 754
Qy 819 GFSIGRLNLISIPVGAKEVQGDIGDSYTYDLSGFFVSDVYRNNPOSTATLVNSPDS--WK 876
Db 755 YFESSDLTNLWPIGKVFERFSDNDIASVNTVLAVPDLVRNSPDKTSLVSPTA 814
Qy 877 IIRGNLSRQAFLLRGSNVYVNSNCELFHGYAMELRGSSRNRYVDGTRKLF 928
Db 815 TKATNLARHAFIVKAGNYLSLSNFIISOQFELKSGSKRTTVNDVDSKIQF 866
RESULT 11
09RB71_CHLVCN
ID 09RB71_CHLVCN PRELIMINARY; PRT; 772 AA.
AC 09RB71; 07BX22;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Pmp_3 (Outer membrane protein 5).
GN Name=pmp_3_2; OederedLocustNames=Cpb0018;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiaceae; Chlamydiales; Chlamydia.
OX NCBI_TaxId=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shiba T., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kunara S., Nakazawa T.,
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TW-183;
 RA Geng M.M., Schumacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 RT other Chlamydia strains based on whole genome sequence analysis."
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BA000008; BAA98226.1; -; Genomic DNA.
 DR EMBL; AE017157; AAP97951.1; -; Genomic DNA.
 DR PIR; H86492; H86492.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR011427; ChlamPMP_M.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 1.
 DR Pfam; PF02415; Chlam_PMP; 6.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP_repeat; 6.
 DR SEQUENCE 772 AA; 82931 MW; 484F5D635801EB CRC64;
 SQ
 Query Match 33.3%; Score 1591; DB 2; Length 772;
 Best Local Similarity 42.7%; Pred. No. 9,7e-80;
 Matches 337; Conservative 146; Mismatches 275; Indels 32; Gaps 14;

Db 644 LQFVAHQBFKQGTAREBFSSRLVNLALPIGRFDKESDQCA-TYNLTGYTVLIV 702
 Qy 859 RNNPOSTATLVMSPDSWKIRGNTLSQAFLRGNNSVYVNSNCELGHYAMELRGSSRY 918
 Db 703 RSNPDCTTLIRISGDSWKTFGTNLAHQALVLRAGNHFCTNSNFARSPQSFELRGSSRY 762
 Qy 919 NVDVGTKLRF 928
 Db 763 NVDLAKAYQF 772
 RESULT 12
 ID P77792 CHLAB
 AC P77792; Q5LSP5;
 DT 01-FEB-1997 (TEMBLrel. 02, Created)
 DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE POMP90B precursor (POMP90A precursor) (Polymorphic outer membrane
 DE protein).
 GN Name=pomp17g; Synonyms=pomp90B; Ordered locusName=CAB598;
 OS Chlamydia abortus
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia
 OC NCBI TaxID=83555;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=526/3;
 RX MEDLINE=89187897; PubMed=9529048;
 RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
 RT "Molecular cloning and characterization of the genes coding for the
 RT highly immunogenic cluster of 90-kilodalton envelope proteins from the
 RT Chlamydia psittaci subtype that causes abortion in sheep."
 RL Infect. Immun. 66:1317-1324(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=526/3;
 RX MEDLINE=96406378; PubMed=8810511; DOI=10.1016/0378-1097(96)00281-9;
 RA Longbottom D., Russell M., Jones G.E., Laine F.A., Herring A.J.;
 RT "Identification of a multigene family coding for the 90 kDa proteins
 RT of the ovine abortion subtype of Chlamydia psittaci."
 RL FEMS Microbiol. Lett. 142:277-281(1996).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=526/3;
 RX PubMed=15837807; DOI=10.1101/gr.3684805;
 RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,
 RA Livingston M., Gerdano-Parraga A.-M., Harris B., Doggett J.,
 RA Omond D., Mungall K., Clarke K., Felwell T., Hance Z., Sanders M.,
 RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.;
 RT "The Chlamydia abortus genome sequence reveals an array of
 RT variable proteins that contribute to interspecies variation."
 RL Genome Res. 15:629-640(2005).
 DR EMBL; U65943; AAC15924.1; -; Genomic DNA.
 DR EMBL; U65942; AAC15922.1; -; Genomic DNA.
 DR EMBL; CR848038; CAH64045.1; -; Genomic DNA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR011427; ChlamPMP_M.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 4.
 DR Pfam; PF02415; Chlam_PMP; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
 KW Complete proteome; Signal.
 FT SIGNAL 1
 FT CHAIN 17 839 Potential.
 SO SEQUENCE 839 AA; 89825 MW; 4581C7CBA7FF4C4 CRC64;
 Query Match 32.7%; Score 1562.5; DB 2; Length 839;
 Best Local Similarity 37.7%; Pred. No. 4.1e-78;
 Matches 362; Conservative 156; Mismatches 290; Indels 151; Gaps 26;

```

OY 1 MKTSLPWLVS-VLAFSCHLOSLAN--EELSPDSEFNGNIDSGTFTPK--TSATYSLT 56
DB 1 MKHVVWFLVSSSL-FASNSLSFANDQFALTPEPDSVNGVNTSEPFQVKEHSSSTYTTCE 59
OY 57 GDFVFEFGKTPYSDSCFKQTTNLTFLNGHSLTGFET-DAGTHAGAAASTTANKNLT 115
DB 60 GNVCSIFAGKDSGAKKSCF-SATDNLTFPLNGYTLCEFDNITTTTASNGAIWVQOGKTLG 118
OY 116 FSGSLISFDSPEPTVYTTGGCTISSAGVNLNIRKLVVAGNSTDGGAIKASFLLT 175
DB 119 ISGSLSCAVCPGCT-----TG-----GAIQKGNLTLLKDN 151
OY 176 GTSGDALFSSNNSSSTKGAIATTAGARIANTGYVRFPLSNIASTSGAIDDEGTSILSNK 235
DB 135 -----TG-----GAIQKGNLTLLKDN 151
OY 236 KFLVPEGNAAKTTGCAICNTYASGSPELIISNNKTLFASVVAETSGAIHAKKLAISGG 295
DB 152 SSVFHKKCSFAEGGAI-QCKSSDAELKINNQNVLVSENSSTSKGAIYADKLTIVSG 210
OY 296 GFTEFLRNNSV-ATPKGALSI--DASGELSLAETGNITFVRN--TLTTGSTDTPKRNA 352
DB 211 GPTLFSSNSVNSGSPKGAISIKDSGECSLTADLGDITPDGKIKITSGSGSTVTRNS 270
OY 353 INISNGKFTELRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNPYQGTILFSGETL 412
DB 271 IDLGT-GKFTLRADGFGIFFYDPT--GGSGDELINNKET--VDYTKIYFSGEKL 324
OY 413 TADELKVADNLKSTTPVSLSGKLLQKGYLTLESTFSGPDAGSLGMDSGTLLSTAG 472
DB 325 SDEEKARAEMLASTNQPIITLSAGSLVTKDVSVAQVTOEAGSTVMDGTTLQTPSS 384
OY 473 ---STTNINGINVDSL---GLKQPVSLTAKGASKVIVSGKLNIDIEGNIVESHMSH 526
DB 385 GGETITLNLNIDINIASLGSGGTSAPAKLATYATASQALITNA-VNLVDAGNAVEPIIAT 443
OY 527 DQFLSLKITVADVDVTNVDISSLIPVPAED-----PMSSEYQFGOMNVNMTTDTATWK 581
DB 444 SKPFLAIYATINA-----STYTOPDTNLTNVPPETHGYQGNMTVWDTETAKT- 493
OY 582 EATATWTKTGVPSPERSALVCTLWGFETDIRSLQOLVEIGATMEHKOGFVWSMTN 641
DB 494 -ATLWEOGTGSPNEBROGPIVPTLMGAFSDLRAIQMLMDISVNGADYHNGFVWSGLAN 552
OY 642 FLHKTGDENRKGFRHTSGGVYVIGSAHTPKDGLTFEAFCHLFAHDKCFIAHNSRTYGG 701
DB 553 FLHSGSDTKRKRFRNSAGYALGVYAKTPSDIFSAACQLFGKQKDYLVSKNNANIYAG 612
OY 702 TLFFGH-SHTLQPONYLRLGRAKFSESAIEKPREIPLADVOVSFHSNDRMETHY--- 757
DB 613 SLIYGHISYWSAMQULLO-----NTIGAPAPLVIANQOLTYCHASNDKMTNMTT 661
OY 758 -----TSLPESEGSNSNECIAGIGLDLPVLSNPHLPFKTFIPQMKVEMVYVSONSFE 812
DB 662 YAPKRTYAEIKGMDGNCDFGVELGATVP-IOTESSLLFDMYSPLFKQLVHTHDDPEKE 720
OY 813 SSSD-CRGFSIGRLNLSIPVGAKFVQGDIGDSTYYDLSGFPVSIVYNNQSTATIAMS 871
DB 721 NNSDGRYPESSNLTNLSLPIGIKFERPANNDTASYHVAASPIVRSNPDCTTSLVS 780
OY 872 PDS--WKIRGNLSRQAFLLRGSNNYVNSNCELFGHAMELRGSRRYNAVVGKFLF 928
DB 761 PDSAAVWTKANNLASFMLQAGNVLISLHNIETISQGFELRGSRRYNAVVDGSKIQF 839

```

RESULT 13
082205 CHLCV PRELIMINARY; PRT: 841 AA.

DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN OrderedLocNames=CCA00624;
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP NCLEOTIDE SEQUENCE.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Neilson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzapple E.K., Khouri H.M., Federova N.B.,
RA Carey H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.D.,
RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
RA Bavoli P.M., Fraser C.M.;
RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae.";
RL Nucleic Acids Res. 31.2134-2147(2003).
DR EMBL; AE016996; AAF05366.1; -; Genomic_DNA.
DR TIGR; CCA00624; -;
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto transpibeta.
DR InterPro; IPR011427; ChlamPMP_M.
DR Pfam; PF03797; Chlamydia_PMP.
DR Pfam; PF07548; Autotransporter; 1.
DR Pfam; PF02415; Chlam_PMP; 4.
DR TIGRFAMs; TIGR01416; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW Complete proteome.
SQ SEQUENCE 841 AA; 90411 MW; 21A9ED16E0D7C65D CRC64;

Query Match 32.3%; Score 1546.5; DB 2; Length 841;
Best Local Similarity 37.3%; Pred. No. 3.2e-77; Matches 137; Gaps 24;
Matches 355; Conservative 163; Mismatches 298; Indels 137; Gaps 24;

```

OY 1 MKTSLPWLVS-VLAFSCHLOSLANBELSPDSEFNGNIDSGTFTPKSAT--TYSLTG 57
DB 1 MKHVVWFLVSSSLFASNSLSFANDQFALTPEPDSVNGVNTSEPFQVKEHSSSTYTTCE 60
OY 58 GDFVFEFGKTPYSDSCFKQTTNLTFLNGHSLTGFET-DAGTHAGAAASTTANKNLT 116
DB 61 GNVCSIFAGKDSGAKKSCF-SATDNLTFPLNGYTLCEFDNITTTTASNGAIWVQOGKTLG 119
OY 117 FSGSLISFDSPEPTVYTTGGCTISSAGVNLNIRKLVVAGNSTDGGAIKASFLLTG 176
DB 120 SGRSLFSCSYCPG--TTEGGAIGQSGVTTSPSNDKIIIFKNCSTEGKAIK----- 169
OY 177 TSGDALFSSNNSSSTKGAIATTAGARIANTGYVRFPLSNIASTSGAIDDEGTSILSNK 236
DB 170 -----CDTGT-----NA 176
OY 237 FLYPEGNAAKTTGCAICNTYASGSPELIISNNKTLFASVVAETSGAIHAKKLAISGG 296
DB 177 ELKEFG-----NXYLLFSGNSSOQEGGAIYAKKLSIISGG 211
OY 297 FTEFLRNNSV-SATPKGALSI--DASGELSLAETGNITFVRNLTTLTGSTDTPKRNA 354
DB 212 PTFSSNNSTKADPKGALCIADADSECLTBANGIIFDGNKIITGTPTP-KRNSID 270
OY 355 IGSNGKFTELRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNPYQGTILFSGETL 414
DB 271 LGSGRKFSQLRANGDFGVFPYDPIANNQSDTDLTEIKKADGA--TYSGRIVFSGEKLTE 328
OY 415 TADELKVADNLKSTTPVSLSGKLLQKGYLTLESTFSGPDAGSLGMDSGTLLSTAG 474
DB 329 DEKQVTDNLKSPFKQPLTVSGSFVLKNGVTSAAKQITQSGGA-IEMDAGTNLTSTEDI 387
OY 475 TITNLGINVDSL---GLKQPVSLTAKGASKVIVSGKLNIDIEGNIVESHMSHDLF- 530
DB 388 SLNVLVINTASLGAGVPLAAGISAEQ-TKNSVTISLNLVDADNGEYEVFVSTTREP 446

```


P71132_CHLAB
ID P71132 CHLAB PRELIMINARY; PRT; 847 AA.
AC P71132; OSLE64;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE POMP91A (Polymorphic outer membrane protein).
GN Name=pmp13G; synonyms=pomp91A; OrderedLocustNames=CA8281;
OS Chlamydia abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83555;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S26/3;
RX MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the
highly immunogenic cluster of 90-kilodalton envelope proteins from the
Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S26/3;
RX MEDLINE=96406378; PubMed=8810511; DOI=10.1016/0378-1097(96)00281-9;
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RT "Identification of a multigene family coding for the 90 kDa proteins
RT of the ovine abortion subtype of Chlamydia psittaci.";
RL FEMS Microbiol. Lett. 142:277-281(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S26/3;
RX PubMed=15837807; DOI=10.1101/gr.3684805;
RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,
Livingstone M., Cerdano-Tarraga A.-M., Harris B., Doggett U.,
Ormond D., Mungall K., Clarke K., Feltwell T., Hance Z., Sanders M.,
Quail M.A., Price C., Barrell B.G., Parkhill J., Longbottom D.;
RT "The Chlamydia abortus genome sequence reveals an array of
variable proteins that contribute to interspecies variation.";
RL Genome Res. 15:629-640(2005).
DR EMBL: U65942; AAC15921.1; -; Genomic DNA.
DR EMBL: CR648038; CAH63731.1; -; Genomic DNA.
DR GO: GO:0019867; C:outer membrane; IEA.
DR InterPro: IPR005546; Auto_transbeta.
DR InterPro: IPR006315; Auto_transbeta.
DR InterPro: IPR011427; ChlamPMP.
DR InterPro: IPR003368; Chlamydia_PMP.
DR Pfam: PF03797; Autotransporter; 1.
DR Pfam: PF02415; Chlam_PMP; 3.
DR Pfam: PF07548; Chlam_PMP; 1.
DR TIGRFAMs: TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs: TIGR01376; POMP_repeat; 3.
KW Complete proteome.
SQ SEQUENCE 847 AA; 90695 MW; 754C958E7F1179E CRC64;
Query Match 32.0%; Score 1532.5; DB 2; Length 847;
Best Local Similarity 37.0%; Pred. No. 1.9e-76;
Matches 357; Conservative 150; Mismatches 302; Indels 157; Gaps 23;
Qy 1 MKTSLPWLVSVAFAFCHLOSLANEE---LSPDDSFNGNIDSGTTP---KTSKTT 52
Db 1 MKHPYVWFLISSSLIVS---NSLYSEEDDKTLTSAHSYNGNTNSEPNPSTNSNGTI 57
Qy 53 YSLGDFVFEYBPG-KGTPLSDFCFQKQTDNTLFLNGHSLTFGFIDA-GTHAGAAASTTA 110
Db 58 YTCGNIGIAIAGLDGSLSSCFITDIGNLSFLDNGYTLCPDNTTQSSHPGALISVGT 117
Qy 111 NKNLTFSGFSLLSPDSBSTVTVTGQGLSSAGVNLNIRKLVVAGNFSADGAIKGA 170
Db 118 NKTLDISGFSLFSCAYCP----- 135
Qy 171 SFLTGTSGDALFSNNSSTKGAIAATTAGARIANNVGYRFLSNIASTSGAIDDEGTS 230
Db 136 -----PGA-----TGY-----GAIKAVGNT 150

Qy 231 ILSNNKFLYFEGNAAKTTGGAICNTKASGSPBLLISNNKTLIPASVNAETSGGAIHAKK 290
Db 151 TIDNNSLVFHKKCSGEGGAIQCKASSEAEIKINNQNLVFAENSSESSGGAIVADKL 210
Qy 291 ALSSGFTFLRNNSVSAIPKGAISI-DASGSLISAETGNTTFYRN-TLTTGTGTDPR 348
Db 211 TIVSGGPTFLSNNSVASBPKGALICIKDSGGCSLTALGDITTFPGNKIKITNGGSPV 270
Qy 349 KRAINIGSNGKFTFLRAAKNHTIFYPDPTSEGTSSDYLKINNGSAGALNPYQGTILPS 408
Db 271 TRNSIDGSSGKTKLNAKEGFGIFFYDPT--GGSDDELINIKQRT---VDYTGAIIVS 325
Qy 409 GETLTADELKVADNLKSFQPVSLGSKLLQKGYTLSTSFSGAGSLGMDSGTTLIS 468
Db 326 GERLSDEKKVAANLKSDFQPLKIGSGSLILKDGYTLERKSPFTQTEGATVWVDLTGLQ 385
Qy 469 TTG---SITITNLGINVDSLG---LKQPVSLTAGASNKVIVSGKMLIDEGNIYES 521
Db 386 TPSSGGETITLTLNDINVASLGGGVAAPPAKVEATTESKVTITNA-VNLVDNGNAIEY 444
Qy 522 HMFSDQLFSLKITYDADVDVTNVDISSLIPVPAED-----PYSEGFOGOMNVNNTDT 576
Db 445 PTLAASQPFPAIEVRSGS-----SGSITKPTTULENTPTPTHGYGQNMVTYTKQGS 496
Qy 577 ATYTKKATATWTKTGFVSPSPERKALVCNTLWGVFTDIBSLQQLVEIGATGMEHKGFVY 636
Db 497 SAQEKATLWEGDTGVSPIBERQSLVPNTLWGSFSDIRAIQVLMIDISVAGADYHNGFVY 556
Qy 637 SSMNTFLHKTGDNKRKGFRTSGGYVIGSAAHPKQDLFPFACHLPADKOCFIAHNS 696
Db 557 SGLGNFLHKSQDTKRFPRNSAGVALGYAQTSPSDVPSAFCQLFGKDKDLVGRNSS 616
Qy 697 RTVGGTFLFGHSHTLQPNYLV---RLGRAKFSESAIEKFPREIPLALDVQVSPSHSDNR 753
Db 617 TVYAGSLYHISYVNTWNTLQNTLG-----AARPLVNLQALACHSNM 663
Qy 754 EHY-----TSLPESGWSNECTIAGGIGLDLPVLNSNPHLPKFTIIPQKVENYV 805
Db 664 KTNMTDTPVAPKTTYSEIKGDMGNDCFGVFCAKAP--IETASLLPDMVSPFYKDLVHA 721
Qy 806 SQNSFPSSSD-GRGSIQGLMLSTPVAKKPVQOIGDSYTYDLDGFFPSDYYVRNPOS 864
Db 722 HODPFKNNSDQGRYFESNNLTNLSMPTIGVKLEKFSHKDTASYNLTLLAVALDIVRSNPD 781
Qy 865 TATLVSPDS--WKIRGNSLROAFLRGSNNYVNSNCELFHYAMELRGSSRNYYVDV 922
Db 782 TATLVSPDSAVVWTTKANMLARHAFILQAGNYLALRNTELPSQFQFELRGSGRTYIDL 841
Qy 923 GTKLRF 928
Db 842 GSKIQF 847

Search completed: November 25, 2005, 14:19:44
Job time : 153.033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:10:51 ; Search time 97.6977 Seconds
(without alignments)
3968.830 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 4782
Sequence: 1 MKTSLPWLVSVAFLFSCHL.....MEIRGSSRNRYNDVGTKEFR 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4782	100.0	928	4 US-10-312-273-115	Sequence 115, App
2	4782	100.0	928	4 US-10-282-122A-54681	Sequence 54681, A
3	4774	99.8	949	4 US-10-289-762-478	Sequence 478, App
4	1855	38.8	928	3 US-09-428-122-2	Sequence 2, Appl
5	1802	37.7	926	4 US-09-738-269-57	Sequence 57, Appl
6	1802	37.7	926	4 US-10-023-437-57	Sequence 57, Appl
7	1794	37.5	928	4 US-10-312-273-33	Sequence 33, Appl
8	1794	37.5	928	4 US-10-503-135-99	Sequence 99, Appl
9	1784	37.3	928	4 US-10-312-273-95	Sequence 95, Appl
10	1763	36.9	930	4 US-10-289-762-470	Sequence 470, Appl
11	1761	36.8	930	4 US-10-312-273-45	Sequence 45, Appl
12	1761	36.8	930	4 US-10-282-122A-54680	Sequence 54680, A
13	1758.5	36.8	927	4 US-10-289-762-472	Sequence 472, App
14	1734	36.3	936	3 US-09-452-380-3	Sequence 3, Appl
15	1734	36.3	936	4 US-10-324-129-3	Sequence 153, App
16	1734	36.3	936	4 US-10-312-273-153	Sequence 54679, A
17	1734	36.3	936	4 US-10-282-122A-54679	Sequence 54679, A
18	1705	35.7	925	3 US-09-452-380-4	Sequence 4, Appl
19	1705	35.7	925	4 US-10-324-129-4	Sequence 4, Appl
20	1562.5	32.7	839	3 US-09-738-269-23	Sequence 23, Appl
21	1562.5	32.7	839	4 US-10-023-437-23	Sequence 23, Appl
22	1535	32.1	746	4 US-10-312-273-19	Sequence 19, Appl
23	1435.5	30.0	841	4 US-10-312-273-139	Sequence 139, Appl
24	1435.5	30.0	841	4 US-10-282-122A-54677	Sequence 54677, A
25	1353	28.3	922	4 US-10-312-273-41	Sequence 41, Appl
26	1353	28.3	922	5 US-10-503-135-98	Sequence 98, Appl
27	1348	28.2	922	3 US-09-886-468-19	Sequence 19, Appl

28	1345	28.1	922	4 US-10-289-762-15	Sequence 15, Appl
29	1286	26.9	643	4 US-10-289-762-474	Sequence 474, App
30	1284.5	26.9	973	4 US-10-312-273-3	Sequence 3, Appl
31	1278.5	26.7	973	4 US-10-352-618-2	Sequence 2, Appl
32	1144.5	23.9	1407	4 US-10-312-273-31	Sequence 31, Appl
33	1144.5	23.9	1407	4 US-10-282-122A-54678	Sequence 54678, A
34	1144.5	23.9	1407	5 US-10-503-135-94	Sequence 29, Appl
35	1132.5	23.7	597	4 US-10-289-762-29	Sequence 29, Appl
36	1130.5	23.6	671	4 US-10-289-762-468	Sequence 468, App
37	1102.5	23.1	1013	4 US-10-467-534-9	Sequence 9, Appl
38	1102.5	23.1	1013	5 US-10-498-327-5	Sequence 5, Appl
39	1102.5	23.1	1013	5 US-10-498-327-81	Sequence 81, Appl
40	1100.5	23.0	1013	5 US-10-498-327-9	Sequence 9, Appl
41	1100.5	23.0	1013	5 US-10-498-327-13	Sequence 13, Appl
42	1100.5	23.0	1013	5 US-10-498-327-93	Sequence 93, Appl
43	1098.5	23.0	1013	5 US-10-498-327-1	Sequence 1, Appl
44	1098.5	23.0	1013	5 US-10-498-327-3	Sequence 3, Appl
45	1098.5	23.0	1013	5 US-10-498-327-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1					
US-10-312-273-115					
; Sequence 115, Application US/10312273					
; Publication No. US20040005667A1					
; GENERAL INFORMATION:					
; APPLICANT: CHIRON SPA					
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE					
; FILE REFERENCE: P025035W0					
; CURRENT APPLICATION NUMBER: US/10/312,273					
; CURRENT FILING DATE: 2002-12-20					
; PRIOR APPLICATION NUMBER: 0016363.4					
; PRIOR FILING DATE: 2000-07-03					
; PRIOR APPLICATION NUMBER: 0017047.2					
; PRIOR FILING DATE: 2000-07-11					
; PRIOR APPLICATION NUMBER: 0017983.8					
; PRIOR FILING DATE: 2000-07-21					
; PRIOR APPLICATION NUMBER: 0019368.0					
; PRIOR FILING DATE: 2000-08-07					
; PRIOR APPLICATION NUMBER: 0020440.4					
; PRIOR FILING DATE: 2000-08-18					
; PRIOR APPLICATION NUMBER: 0022583.9					
; PRIOR FILING DATE: 2000-09-14					
; PRIOR APPLICATION NUMBER: 0027549.5					
; PRIOR FILING DATE: 2000-11-10					
; PRIOR APPLICATION NUMBER: 0031706.5					
; PRIOR FILING DATE: 2000-12-22					
; NUMBER OF SEQ ID NOS: 664					
; SOFTWARE: SeqMan99, version 1.02					
; SEQ ID NO 115					
; LENGTH: 928					
; TYPE: PRT					
; ORGANISM: Chlamydia pneumoniae					
US-10-312-273-115					
Query Match					
Best Local Similarity 100.0%; Pred. No. 4.1e-307;					
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MKTSIPWLVSVAFLFSCHL	SIANEELISPPDSFNGNIDSGTFPKTSATYSLTGDF	60	
Db	1	MKTSIPWLVSVAFLFSCHL	SIANEELISPPDSFNGNIDSGTFPKTSATYSLTGDF	60	
Qy	61	FYEPEKGPLSDSCFKQTTDNLTFPGNGHSILTFGFI	DAGTAGAAGAASTTANKLTFSGPS	120	
Db	61	FYEPEKGPLSDSCFKQTTDNLTFPGNGHSILTFGFI	DAGTAGAAGAASTTANKLTFSGPS	120	
Qy	121	LISFSSSTVTYTGQGLTSSAGVNLNIRKLVAAGNFT	ADGGAIGASFTLGTSGD	180	
Db	121	LISFSSSTVTYTGQGLTSSAGVNLNIRKLVAAGNFT	ADGGAIGASFTLGTSGD	180	

```

Qy 181 ALFSNNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGGAIIDDEGTSILSNKFLYF 240
Db 181 ALFSNNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGGAIIDDEGTSILSNKFLYF 240
Qy 241 EGNAAKTGGAI CNTKASGSPDLII SNKTLIFASNAETSGGAIHAKKLALSSGGTTF 300
Db 241 EGNAAKTGGAI CNTKASGSPDLII SNKTLIFASNAETSGGAIHAKKLALSSGGTTF 300
Qy 301 LRNNVSATPKGAIISIDAGSELISAETGNITFVRNTLTTSSTDPKRNAINIGSNGK 360
Db 301 LRNNVSATPKGAIISIDAGSELISAETGNITFVRNTLTTSSTDPKRNAINIGSNGK 360
Qy 361 FTBLRAAKNHTIFPYDPTSEGTSSDYLKINNSAGALNPYOGTILFSGETLTADDELKVA 420
Db 361 FTBLRAAKNHTIFPYDPTSEGTSSDYLKINNSAGALNPYOGTILFSGETLTADDELKVA 420
Qy 421 DNLSKSTFQPVSLSGGKLLQKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNNG 480
Db 421 DNLSKSTFQPVSLSGGKLLQKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNNG 480
Qy 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDQLFSLKITVDAD 540
Db 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDQLFSLKITVDAD 540
Qy 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMVNMWTTDTATNTKEATATWTGTFVPSPERKS 600
Db 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMVNMWTTDTATNTKEATATWTGTFVPSPERKS 600
Qy 601 ALVNCNTLMGVTFTDIRSLQOLVEIGATGMEHKQGFVWSMTNFKHKTGDENRKGRHTSGG 660
Db 601 ALVNCNTLMGVTFTDIRSLQOLVEIGATGMEHKQGFVWSMTNFKHKTGDENRKGRHTSGG 660
Qy 661 YVIGGSATPKDDI.FTFAFCHLPARDKOCFTAHNNSRTYGGTLPFKHSHTLQOPNYRLG 720
Db 661 YVIGGSATPKDDI.FTFAFCHLPARDKOCFTAHNNSRTYGGTLPFKHSHTLQOPNYRLG 720
Qy 721 RAKSESASIEKFPREIPLALDVQVFSHSDNRMEHTYSLPESBSGSWNECIAGIGIDL 780
Db 721 RAKSESASIEKFPREIPLALDVQVFSHSDNRMEHTYSLPESBSGSWNECIAGIGIDL 780
Qy 781 PFVLSNPHLPFKTPIPOKKEVEMVYVQNSPFESSSDGSGFISIGRLNLSIVYGAKFVQGD 840
Db 781 PFVLSNPHLPFKTPIPOKKEVEMVYVQNSPFESSSDGSGFISIGRLNLSIVYGAKFVQGD 840
Qy 841 IGDSTTYLSCGFVSDVRRNPQSTATILVMSPDMSKLRGNLSROAFILRGSNNYVYNSN 900
Db 841 IGDSTTYLSCGFVSDVRRNPQSTATILVMSPDMSKLRGNLSROAFILRGSNNYVYNSN 900
Qy 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928
Db 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928

RESULT 2
US-10-282-122A-54681
; Sequence 54681, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

```

```

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54681
; LENGTH: 928
; TYPE: PR
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54681

Query Match 100.0%; Score 4782; DB 4; Length 928;
Best Local Similarity 100.0%; Pred. No. 4,1e-307;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKSISPVVSVSLASCHLOSLANBELSPDSEFNGNIDSGTFRTKTSATYSLGDPF 60
Db 1 MKSISPVVSVSLASCHLOSLANBELSPDSEFNGNIDSGTFRTKTSATYSLGDPF 60
Qy 61 FYEPGKGTPLSDSCFKQTTDNLTFLNGHSLTFGFLDAGTHAGAASTTANKMLTFESGS 120
Db 61 FYEPGKGTPLSDSCFKQTTDNLTFLNGHSLTFGFLDAGTHAGAASTTANKMLTFESGS 120
Qy 121 LLSFDDSPSTVTVTGQGTSLSSAGVNLNIRKLVAGNFTADGAIKGAFLTGTSGD 180
Db 121 LLSFDDSPSTVTVTGQGTSLSSAGVNLNIRKLVAGNFTADGAIKGAFLTGTSGD 180
Qy 181 ALFSNNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGGAIIDDEGTSILSNKFLYF 240
Db 181 ALFSNNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGGAIIDDEGTSILSNKFLYF 240
Qy 241 EGNAAKTGGAI CNTKASGSPDLII SNKTLIFASNAETSGGAIHAKKLALSSGGTTF 300
Db 241 EGNAAKTGGAI CNTKASGSPDLII SNKTLIFASNAETSGGAIHAKKLALSSGGTTF 300
Qy 301 LRNNVSATPKGAIISIDAGSELISAETGNITFVRNTLTTSSTDPKRNAINIGSNGK 360
Db 301 LRNNVSATPKGAIISIDAGSELISAETGNITFVRNTLTTSSTDPKRNAINIGSNGK 360
Qy 361 FTBLRAAKNHTIFPYDPTSEGTSSDYLKINNSAGALNPYOGTILFSGETLTADDELKVA 420
Db 361 FTBLRAAKNHTIFPYDPTSEGTSSDYLKINNSAGALNPYOGTILFSGETLTADDELKVA 420
Qy 421 DNLSKSTFQPVSLSGGKLLQKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNNG 480
Db 421 DNLSKSTFQPVSLSGGKLLQKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNNG 480
Qy 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDQLFSLKITVDAD 540
Db 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDQLFSLKITVDAD 540
Qy 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMVNMWTTDTATNTKEATATWTGTFVPSPERKS 600
Db 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMVNMWTTDTATNTKEATATWTGTFVPSPERKS 600

```

QY 601 ALVNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSWMTNPLAKTGDENRKGFPHTS6 660
DB 601 ALVNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSWMTNPLAKTGDENRKGFPHTS6 660
QY 661 YVIGSSAHTPKDPLTPAFCHLFARDKDCFIANNSTRYGGTLFPKSHHTLOPONYLRIG 720
DB 661 YVIGSSAHTPKDPLTPAFCHLFARDKDCFIANNSTRYGGTLFPKSHHTLOPONYLRIG 720
QY 721 RAFFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 780
DB 721 RAFFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 780
QY 781 PVLNSPHPLFKTFIPQMKVEMVYVONSFFESSDGRGFSIGRLNLSIPVGAKEVQGD 840
DB 781 PVLNSPHPLFKTFIPQMKVEMVYVONSFFESSDGRGFSIGRLNLSIPVGAKEVQGD 840
QY 841 IGDSYTYDLSGFFVSDVYRNNPOSTATLVMSPDMSKIRGNSLRQAFLRGSNVYNSN 900
DB 841 IGDSYTYDLSGFFVSDVYRNNPOSTATLVMSPDMSKIRGNSLRQAFLRGSNVYNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 3

US-10-289-762-478
; Sequence 478, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 478
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...949
; OTHER INFORMATION: Xaa=unknown or other
; US-10-289-762-478

Query Match 99.8%; Score 4774; DB 4; Length 949;
Best Local Similarity 99.9%; Pred. No. 1.4e-306;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTISPMVLVSVLAESCHLOSANBELASPDSFNGNIDSGTFPTKTSATYVSLGDFV 60
DB 22 MKTISPMVLVSVLAESCHLOSANBELASPDSFNGNIDSGTFPTKTSATYVSLGDFV 81
QY 61 FYRPGKTPISDSCKFQTTDNLTFLNGHSLTRGFIDAGTHAAGAASTTANKULTS6GS 120
DB 82 FYRPGKTPISDSCKFQTTDNLTFLNGHSLTRGFIDAGTHAAGAASTTANKULTS6GS 141
QY 121 LLSFDSSTPTVTTGGTSSAGAVNLENRKLVAAGNFTAGGAIKGSFLLTGTSGD 180
DB 142 LLSFDSSTPTVTTGGTSSAGAVNLENRKLVAAGNFTAGGAIKGSFLLTGTSGD 201
QY 181 ALFSNNSSSTKGAIATTAGARIANTGYRFLSNIASTSGAIDDEGTSILSNKFLVF 240
DB 202 ALFSNNSSSTKGAIATTAGARIANTGYRFLSNIASTSGAIDDEGTSILSNKFLVF 261
QY 241 EGNAAKTTGAIANTASGSPILLISNNKTLIFASNAEISGAIHAKKIALSSGGFTEP 300
DB 262 EGNAAKTTGAIANTASGSPILLISNNKTLIFASNAEISGAIHAKKIALSSGGFTEP 321

QY 301 LNNVSSATPKGGAISIDASGELSASAEIGNITFPVRNLTITGSDTPRKRNAINISNGK 360
DB 322 LNNVSSATPKGGAISIDASGELSASAEIGNITFPVRNLTITGSDTPRKRNAINISNGK 381
QY 361 FTLELPAKKNHTTFPDPTTSEGTSSDVLTINNKGALNPYGGTLFSGEITLTABELKVA 420
DB 382 FTLELPAKKNHTTFPDPTTSEGTSSDVLTINNKGALNPYGGTLFSGEITLTABELKVA 441
QY 421 DNLKSSFTQPVSLSGKLLQKGVTESTSPSOEAGSLGMDSGTTLSTAGSIITYNIG 480
DB 442 DNLKSSFTQPVSLSGKLLQKGVTESTSPSOEAGSLGMDSGTTLSTAGSIITYNIG 501
QY 481 INVDSLGLKOPVSLTAKGASRVIVSGKLNLIIDEGNIESHMFSDQLFSLKITTVDAD 540
DB 502 INVDSLGLKOPVSLTAKGASRVIVSGKLNLIIDEGNIESHMFSDQLFSLKITTVDAD 561
QY 541 VDTNNDISLIVPAEDPSEYGFQGNVNMVTTDTATNTEKATATWKTGVPSPERKS 600
DB 562 VDTNNDISLIVPAEDPSEYGFQGNVNMVTTDTATNTEKATATWKTGVPSPERKS 621
QY 601 ALVNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSWMTNPLAKTGDENRKGFPHTS6 660
DB 622 ALVNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSWMTNPLAKTGDENRKGFPHTS6 681
QY 661 YVIGSSAHTPKDPLTPAFCHLFARDKDCFIANNSTRYGGTLFPKSHHTLOPONYLRIG 720
DB 682 YVIGSSAHTPKDPLTPAFCHLFARDKDCFIANNSTRYGGTLFPKSHHTLOPONYLRIG 741
QY 721 RAFFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 780
DB 742 RAFFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 801
QY 781 PVLNSPHPLFKTFIPQMKVEMVYVONSFFESSDGRGFSIGRLNLSIPVGAKEVQGD 840
DB 802 PVLNSPHPLFKTFIPQMKVEMVYVONSFFESSDGRGFSIGRLNLSIPVGAKEVQGD 861
QY 841 IGDSYTYDLSGFFVSDVYRNNPOSTATLVMSPDMSKIRGNSLRQAFLRGSNVYNSN 900
DB 862 IGDSYTYDLSGFFVSDVYRNNPOSTATLVMSPDMSKIRGNSLRQAFLRGSNVYNSN 921
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 922 CELFGHYAMELRGSSRNRYNDVGTCLRF 949

RESULT 4

US-09-428-122-2
; Sequence 2, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Mardin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-428-122-2

Query Match 38.8%; Score 1655; DB 3; Length 928;
Best Local Similarity 42.7%; Pred. No. 1e-113;
Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;

Db 766 WGNDTLGLTSTVPIPVFSS--SIFDSYAPFAKLQVYVAHODDFKEPTTEGRVFESSDL 823
Qy 826 LNSTIPVAKFVQGDIDGSTYDLSGFVSDVYRNPNQSTATLLVMSPDMSKIRGNLSRQ 885
Db 824 LNVSVPIGIFKEKLSYGBRSAYDLTLMYIPDYVRHNSCMTGLAINDVSLTTATNLARQ 883
Qy 886 AFLLRGSNNYVNSNCELFGHYAMELRGSSRRNVNDVGTCLRF 928
Db 884 AFLVRAGNHIALTSGVEMFSQGFELRSSSRNVNDLGAQVAF 926

RESULT 6
US-10-023-437-57
; Sequence 57, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: US/10-023-437
; CURRENT APPLICATION NUMBER: US/10-023-437
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225, 839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 926
; TYPE: PR1
; ORGANISM: Chlamydia psittaci
US-10-023-437-57.

Query Match 37.7%; Score 1802; DB 4; Length 926;
Best Local Similarity 40.8%; Pred. No. 3.2e-110;
Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;
Qy 1 MKTSLIPWVYSSVLA--FSCHLQSLANEELSPDSDNGNIDGSTFPKTSATT-----YS 54
Db 1 MRBSLYKILISLTLLPDISFHSQLAHEVALTOESILIDAN---GAFSPDSTAGGTIYN 57
Qy 55 LTGQVFYEPGKGPLSDSCFKQTTDLTLFGNGHSLTFGFIADGAGAAATANKNL 114
Db 58 VESDISLVDVGQTAALSSAFVQTAADNLTKGNHSLSTINAAAGNPAGINVTADKIL 117
Qy 115 TFGSFFSLSPDSSPTVTGQGLTSSAGGVNLENIRKLVVAGNFTADGAIKGAFFL 174
Db 118 TLVDFSLSTFKRECSLSLVNKGKMGSGALNLANNASILFDQVYSAENGAISCKAFSL 177
Qy 175 TGTSGDALFSNNSSTYCGAIAATTAGRIANNGTGYAFPLSNIASTSGCAIDDECTSLSN 234
Db 178 TGSSKEISFTTNSYAKKGAIATAGIALSDNCGTIRFSGNTAVNSGAVYSEASMTIAG 237
Qy 235 NKFLYPEGNNAKTT---GGAICNTKASGSPBELIISNNKTLIFASNVVAETSGAIAHKKL 290
Db 238 NNHVAFFNNNAVSGSSDCCGAIHCKTGSAPTLTIRNKVLIPEENTSSAKGAILYDKL 297
Qy 291 ALSSGGTFEFLRNNVSSATPKGAISIDAGELSLAETGNITFVRNTLLTTSSTDTPKR 350
Db 298 ILTSGGPTAFINNKVTATPKGAIIGIAANGEGSLTEHGDITF-DNNLWATQDNATIKR 356
Qy 351 NAINIGSNGKFTELRAAKNHTIFPYDPTSEGTSSDVCLKINNSAGALNYOQTILFSGE 410
Db 357 NAINIEGNGKFTVNLRAASGKTIISFYDPTVEGNAAADLLTINKEGD--KTYNGIIFSGE 414
Qy 411 TLTADELKVADNLSKSTFOPVSLSGKLLLOKGVLTLESTSPQBSGLMDSGTTLSTT 470
Db 415 KLTBEQAAVADNLTITPTPTTLAAGELVLRSGVEAKVIVQTAGSLIMDACTKLSAK 474
Qy 471 AGSITITNLGINVDSLGLKQPVSLTAKASNKVTSGLMLIDIENIYESHMFSDOLF 530

Db 475 TEDATLTNLAINPNTLDGKFAVNDVAAGKVTLLSGAIGVIDPTGKFEYENHKLNDTLAL 534
Qy 531 SLUKITVDADVDTNVDISSLIPVPAEDPNSSEYGFQGMVNNVTTDPATNTKEATA--TWT 588
Db 535 GGIQLSGKSSV-TTINVPESHVGVAE--THYGYQNSVSVYKDNNSDPKQTALFTPN 590
Qy 589 KTGVPSPERKALVNCNTLMGVFTDIRLSLOQLVEIGATG-MEHKQGFVWSMTNPLHKTG 647
Db 591 KTGYPNPNRRAPLVNLNLSMGSFIDRSIQDVLERSVDSILFTRRLQWVSGIGNFPHKOR 650
Qy 648 D-ENRKGFRHTSGGYIGGSAATPKDULTFPAFCHLPADKXCFLAHNNSRTYGTCLFPRK 706
Db 651 MAENRK-FRHISSGYLGAITNTSREDLSLVAFCQLFADKXYLVSKNANYAGSVYQQ 709
Qy 707 HSHITLQPNVYLRGRKAFSESAIEKPRRIPLADQVFSFSDRMETHYTSLPSESGS 766
Db 710 HSKFDDTLRLFRNG---PNTCCSGFSKELPFLDAQIYCHTANNMTTSYIDYEPVKS 765
Qy 767 WSNECIAGIGLDLPF-VLSNPHPLFKTEIPQMKVEMVYVNSQNSPFESSDGRGFSIGRL 825
Db 766 WGNDTLGLTSTVPIPVFSS--SIFDSYAPFAKLQVYVAHODDFKEPTTEGRVFESSDL 823
Qy 826 LNSTIPVAKFVQGDIDGSTYDLSGFVSDVYRNPNQSTATLLVMSPDMSKIRGNLSRQ 885
Db 824 LNVSVPIGIFKEKLSYGBRSAYDLTLMYIPDYVRHNSCMTGLAINDVSLTTATNLARQ 883
Qy 886 AFLLRGSNNYVNSNCELFGHYAMELRGSSRRNVNDVGTCLRF 928
Db 884 AFLVRAGNHIALTSGVEMFSQGFELRSSSRNVNDLGAQVAF 926

RESULT 7
US-10-312-273-33
; Sequence 33, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035MO
; CURRENT APPLICATION NUMBER: US/10-312-273
; CURRENT FILING DATE: 2002-12-20
; PRIOR FILING DATE: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 33
; LENGTH: 928
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-33

Query Match 37.5%; Score 1794; DB 4; Length 928;
Best Local Similarity 42.7%; Pred. No. 1.1e-109;
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;
Qy 1 MKTSLIPWVYSSVLA--FSCHLQ--SLANEELSPDSDNGNIDGSTFPK-----KTSAT 51
Db 1 MKSSLHPLISSLAPLPSLNSAFPAVAVEINLGPNTSPSG--PETYTPPAQQTNAQDT 57

Qy	52	TYSLTDGVFEYBEQKOTPLPDSQCFQOTDNJLFLFNGHSLTFEGFDGTHAGAASTTAN	111
Db	58	IYULTDGVSTYTAGSPFTALTASCPEKETTGNLSFQHGVOPLQONIDAGANC-PTYNAN	116
Qy	112	KNLTFSGFSLLSDFSDSPFTVTYGOQYSSAGVNLNIRKLVAAFNSTADGAIKGA	171
Db	117	KLTFSGGFYSLYS--TQTNATGTGGAIKSTGACISQNSCYFGQMFNSNGGALGSS	174
Qy	172	FLLTGNISGDLFENNSSSTKGAIAFTTGARLANNQTVYRFLSNIASTSGGALDDEGTSI	231
Db	175	ISLS-LAPNLTFAKMATQKGAISTGCIITNNLNSASSENTAANNGAIYTEASSF	233
Qy	232	LSNNKFLYFEGN---AAKTTGAI-CNTYASGSPELIISNNKTLIFASNAETSGAIIA	287
Db	234	ISSNKAIISFTNNSVTATSATGAIYCSSPSAKPVLTLSDNGELNFTGNTAITSGAIYT	293
Qy	288	KKLALSSGGTELELRN-VSSATPKGAIISDASELISLAETGNTFVNTLT--TGT	345
Db	294	DNVLSSGGTFLPKNNASIDTAPALCGAIALDSSLSLALGDIITFEGTVVKGASS	353
Qy	346	DPEKRAINIG-SNGFTELEAKAKNHTTFEYDPTISEGTS--SDVLKTNNSAGALNPQ	402
Db	354	QTTTRNSINIGNNAKIYOLRASQNTIYFYDPIITSTIALSDALNNGPDLGNAYQ	413
Qy	403	GTLTFSGEITLTADELKVDNLKSSFTQVPSYLSGGKLLIQKYTLESTSPSQEAGSLIGMD	462
Db	414	GTVFSGEKLSEAEAEADNLKSTIOQPLTLGQGLSKSGVTLVAKFSQSPGSTLMD	473
Qy	463	SGTLTSTTASITITNLGINVDSLGKQVSLTAAGASNKIVYSGKNLJIEENIYESH	522
Db	474	AGTTLLETADG-TITNNLVANDSLKKTAKATIKAQASQYTLTSSLSLVDPSSNYEDV	532
Qy	523	MFSHDQFLSLKKTVDADVDTNVDISSLIPVAEDPNSEYGFQOGWNVMTDTATNKE	562
Db	533	SNMNPQVFSCLTLT--ADDPANHITDLADPLEKNPIHMGYQWNAALSMQEDATSKA	590
Qy	583	ATATMTGTGVPBPBKRSALVONTLNGVTTDIRSQOYVEIGATGEMHKQSPFWSSMNF	642
Db	591	ATLTWTGTGNPNPBERGTLVANTLNGSFVDVRSIOQLATKVRQSOCTTRGIMGEGISNF	656
Qy	643	LHKGTGDNRGKPHTSQGYVIGGASATPTDDLTFAFCHLFARDXCEFIANNSTRYQGT	702
Db	651	FHKOSTKINGPFIHISAGVYVAGTTTLASDNILITAFQCLPEKDRDHPINNRASAYAS	710
Qy	703	LFFHGHTLOPONTLRLGRAKSSESAIEKFPREIPLADVQVSESHSDNRKETHYTSPE	766
Db	711	LHLQHTLTLSPSLIR--LPGSES-----EQVLPFAQISTYSYKNTKTKYTTAPK	761
Qy	763	SEGSWSNECIAGGIGDLPEVLNSNPHLPFKTFIPQKVMVYVONSSEFSSSD-GRGFS	821
Db	762	GESWNYDGCALBELASLPHLTALSHGULPHAAYPPIKVDASTIHDOSKENTLIVNSFD	822
Qy	822	IGRLNLISFVGAKFVQGDIGDSYTYDLSGFVSDVYRNNPOSTALTYVMSPDSKIRGN	881
Db	822	SGDLINYSVPIGITFEERFSNERASYEATYIVADYVRNPPCITTALLINNTSMKTTGTN	881
Qy	882	LSRPAFLRSNNVYVNSNCELFCHAMELRGSSRVNVDTGTXRF	928
Db	882	LSRQAGIRAGIYAFPNLEVISNLSMEIRGSSRYNADLGGKQF	928

```

: PRIOR FILING DATE: 2003-02-13
: PRIOR APPLICATION NUMBER: GB-0203403.1
: PRIOR FILING DATE: 2002-03-13
: NUMBER OF SEQ ID NOS: 181
: SOFTWARE: Sequn199, version 1.02
: SEQ ID NO 99
: LENGTH: 928
: TYPE: PR1
: ORGANISM: Chlamydia pneumoniae
: US-10-503-135-99

```

Query Match	37.5%	Score 1794	DB 5	Length 928
Best Local Similarity	42.7%	Pred. No. 1	1e-109	
Matches 404	Conservative 152	Mismatches 353	Indels 38	Gaps 17

```

0Y 1 MKT31PMVLVSUAFSCHLO---SLANEELLSPDOSFNONIDSGFTP-----KTSAT 51
Db 1 MKSS1HMFELISS1ALPLSLN1FSAFPAVAVEINLGP1NSFSG--PG1YTPPAQ1T1NADGT 57
0Y 52 TYS1LTGVDFVEPEGK7P1SDSCFCQ1OTD1N1FL1CNGH1SLTFEG1DACTHGA1A1STAN 111
Db 58 IYN1LTGVST1NNA1SP1AL1TAS1CRETT1GN1SPQHG1Q1P1LQ1N1IDA1NC--T1F1NT1A1N 116
0Y 112 KNL1TFSG1LL1SPD1SS1PST1VT1TQ1GL1S1AGV1N1EN1RKL1VA1GN1ST1AD1G1AK1AS 171
Db 117 KLS1FSFG1SY1SL--1Q1T1N1AT1TG1G1AK1S1G1AC1S1Q1GN1YC1FG1Q1NF1S1ND1G1AL1Q1G1S 174
0Y 172 FL1L1GT1SD1AL1F1SN1SS1ST1KG1AL1AT1TGA1RI1ANN1TV1R1FL1SN1AS1T1SG1A1ID1EG1SI 231
Db 175 I1SL1-L1N1NL1F1PA1K1K1AT1Q1K1G1AL1Y1TG1G1IT1N1N1L1N1S1AS1F1S1E1N1T1A1N1NG1A1Y1E1AS1F 233
0Y 232 L1SN1K1F1E1F1E1G1N1---A1A1K1TG1G1A1-C1N1TK1AS1G1S1P1E1L1I1SN1K1T1L1F1A1N1V1A1E1T1SG1A1I1A 287
Db 234 I1SN1K1A1F1I1N1SV1AT1AT1G1AL1Y1CS1TS1A1K1P1V1L1T1SD1NG1E1N1F1G1T1A1T1T1SG1A1Y1T 293
0Y 288 K1LA1ISS1G1F1E1PL1RN--V1S1AT1PK1GA1I1S1D1AG1E1LS1A1E1T1G1N1IT1V1R1N1T1LT--T1G1T 345
Db 294 DNL1V1SS1G1P1FL1K1N1SA1ID1T1A1P1UG1A1I1A1D1SG1E1LS1A1L1G1G1D1T1E1G1N1V1V1G1A1SS1 353
0Y 346 D1P1K1N1A1N1IG--S1N1G1K1F1E1L1A1A1K1N1HT1F1P1D1P1T1S1E1G1S--S1V1Y1K1I1N1NG1A1G1AL1N1P1Q 402
Db 354 Q1T1T1K1N1S1I1N1G1N1T1AK1I1V1Q1L1P1AS1Q1C1N1T1Y1F1D1P1T1T1S1I1T1A1L1S1D1L1N1G1P1L1AG1N1P1AY1Q 413
0Y 403 GT1L1P1SG1E1T1L1A1D1E1L1K1V1AD1N1K1S1E1T1Q1P1VS1I1SG1K1L1K1Q1V1T1E1S1T1F1S1Q1E1AG1L1G1ND 462
Db 414 GT1V1SS1G1K1L1E1A1E1A1E1AD1N1K1ST1I1Q1P1L1T1A1G1G1L1S1K1G1V1T1A1K1S1F1S1Q1P1G1ST1L1MD 473
0Y 463 S1G1T1L1ST1AG1S1I1T1T1N1G1I1N1D1S1L1G1K1P1V1S1L1T1A1G1AS1N1K1Y1V1S1G1K1L1I1D1E1G1N1Y1E1H 522
Db 474 A1G1T1E1T1A1D1G--I1T1N1N1L1V1N1D1S1L1K1E1T1K1AT1L1K1A1Q1A1Q1V1L1S1L1S1I1V1D1S1G1N1Y1E1V 532
0Y 523 M1E1SH1O1L1S1L1K1I1T1D1A1D1V1D1N1V1D1S1L1P1V1A1E1D1P1N1S1E1V1Q1G1Q1G1O1M1N1V1T1D1T1A1T1K1E 582
Db 533 S1W1N1N1Q1V1S1C1L1LT--A1D1P1A1N1I1H1T1D1L1A1D1L1E1K1N1P1H1M1G1I1Q1G1N1W1A1L1S1Q1E1D1I1T1K1S1A 590
0Y 583 A1T1A1T1K1G1F1V1S1P1E1R1K1A1L1V1C1N1T1L1M1G1F1T1D1R1S1L1Q1V1E1A1T1G1A1M1E1H1K1O1G1F1W1A1S1M1T1F 642
Db 591 A1T1L1T1K1G1Y1N1P1E1R1G1I1V1A1N1T1L1M1G1S1V1D1V1R1S1I1Q1L1V1A1T1K1V1R1S1Q1E1T1R1G1I1M1C1E1S1N1F 650
0Y 643 L1H1K1T1O1D1E1N1K1G1F1R1H1T1S1G1Y1V1T1G1S1A1H1T1P1K1D1L1F1A1F1C1H1L1A1R1D1O1C1F1A1H1N1S1R1Y1G1T 702
Db 651 F1H1K1D1S1T1K1N1G1F1R1H1S1A1G1V1G1A1T1T1L1S1D1N1I1T1A1F1O1L1F1E1K1D1H1F1N1K1R1A1A1Y1A1S 710
0Y 703 L1E1F1K1S1H1T1L1Q1P1O1N1Y1L1R1G1A1K1S1E1A1I1E1K1F1P1E1I1P1A1D1V1O1S1F1S1H1D1R1M1E1T1H1S1L1P1E 762
Db 711 L1H1L1Q1A1T1L1S1E1P1S1L1R1Y--L1P1E1S1E1-----E1Q1V1L1D1A1Q1I1S1Y1S1K1N1T1K1T1Y1T1Q1A1K 761
0Y 763 S1E1G1S1N1E1C1I1A1G1I1D1L1P1F1V1S1N1H1P1L1F1K1P1I1P1M1K1E1M1V1N1V1S1Q1N1S1P1E1S1S1D--G1R1G1S 821
Db 762 G1E1SS1Y1N1O1G1A1L1E1L1S1L1P1H1T1A1L1S1H1E1G1L1F1H1A1V1F1P1K1E1A1S1Y1I1H1Q1D1S1F1E1R1N1T1T1V1L1R1S1P1D 821
0Y 822 I1G1R1L1N1S1I1P1V1G1A1K1V1Q1G1D1G1S1Y1Y1D1S1G1F1V1S1D1Y1R1N1P1O1S1T1A1T1L1V1S1P1D1S1W1K1R1G1N 881

```



```
Db      822 SGDLINVSPIGITEFPERSRNERASYATVIYADVRRKNPDCTTALLINNTSKTTGTN 881
Qy      882 LSRQAFLLRGSNNVYNSNCELFGHYAMELRGSSRNINVDVGTURF 928
      882 LSRQAGIGRAGIFAFASPNLEVTSLNLSMEIRGSSRSRYNADLGKRFQF 928

RESULT 9
US-10-312-273-95
; Sequence 95, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 95
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-95

Query Match      37.3%; Score 1784; DB 4; Length 928;
Best Local Similarity 40.4%; Pred. No. 5e-109;
Matches 385; Conservative 174; Mismatches 343; Indels 52; Gaps 18;

Qy      1 MKTSIPWVYVSSVYA--FSGHLOSANBELSPDSDNGNIDSGTFPPKTSAT--TYSLT 56
Db      1 MKQFSLVLSSTLACTSCSTVFPAATAENIGPDSFDGSTNTGTYPKNATTGIDYTLT 60
Qy      57 GDVFFYEPGKGTPLSDSCFKQTTDNITFLGNHSLTFGFTDAGTHAGAASTTANKULTF 116
Db      61 GDTITQNLGDSALTKKCFSDTHESLSFAGKGYSLSLNKKSAE--GALSVTTDKRLSL 119
Qy      117 SGFSLISFDDSPSTVT--GQGTLSAGAGVNLNIRKLVAAGNFSTADGAIKGSFLL 174
Db      120 TGFSSLTFLAPASVITTPSGKAVKCGDLPDNNGTILFKQDYCEHNGALSTKULSL 179
Qy      175 TGTSGDALFSNNSSST--KGAIAITTAGARIANNTCYVAFSLNIASTSGAIDDEGTSI 231
Db      180 KNSGTGISFEGNKSATGKKGAIICATGTVDITNNTAPLTFSSNIIAAGAIINSTGNC 239
Qy      232 LSNKKFLYFEGNAKTT--GGAICNTKASGSPDLISNNKTLIPASNVAETSGAIIHAK 288
Db      240 ITGNTSLVFSENSVTATAGNGAL-----SGDADVTISNGSVTFSGNOAVANGAIYAK 294
Qy      289 KLAIS--GGFTBLRNVSATP--KGAISIDASGELSLAETGNITFVRNTLTJTTGST 345
Db      295 KLTLASGGGVSPFLITIIVOGTTAGNGAISIILAGCSLSABAADITFGNAIVAT--TP 353
Qy      346 DTPKRNAINSGNCKFTELAANKHTIFFYDPTTSE--GTSSDVLKINNSAGALNPYG 403
Db      354 QTTKRNSIDIGSTAKTINLPAISGHSIFPYDPTTANTAADSTDTLMLNKADAGNSTDYS 413
```

```
Qy      404 TILFSGETITABELKADNLIKSFPTQVSLGGKLLQKGVLTLESTSFQEGAGSLIGMS 463
Db      414 SIYFSGEKLSEDBAKVADNLTSLKQPVTLTAGNLVLKQGVTLTDGTFQTAGASSYIMDA 473
Qy      464 GTTLSTAGSITITNLGINVDSIGLKQPVSLTRKASNKYIVSGKLNLDIBENITESM 523
Db      474 GTTLKASTBEVTLTGISIPVDSLGBGKAVIYAASAKVVALSGPILLDNOGAAENHD 533
Qy      524 FSHDQFLSLKITVDADVDTNVDISLIPVPAEDPSEYGFQOGQVNVNMTTTPAT--NPK 581
Db      534 LKGTQDFSVQJSA--LGTATTTDVPA---VPVYATPTHYGYQGTMGMTAVDDTASTPKTK 589
Qy      582 EATATWTKTGFVSPERKALVNTLMGVFTDIRSLQOLVEIGATGMEHKQGFWSSMTN 641
Db      590 TATLAATNTGYLPENPFRQGPLVNSLWGSFSDIQAIQVIERBALTLCSDRGFMAAGVAN 649
Qy      642 FLHKTDENRKGFRHRTSGGVYIGGSAHTRKDLPFTAFCFLPARBDCITAHNSSTYGG 701
Db      650 FLDKDKKGRKRKRHKSGGYVIGGAQTCSENLISPAFQULFGSDKDFLAKNHTTYAG 709
Qy      702 TLFFKSHTLQPNVYRLGRAKFSESAIKFP--REIPLADVQVSFSDNRMETHYT 758
Db      710 AFYIQHTEC-----SGFICGLDLKLPSSMSHKPLVLEGQLAHVSHNDLTKYT 759
Qy      759 SLPESEGSNSNECIAGIGLDLPFVLSNHP---LFKTFIPQMKVEMVYVSGNSPFESS 814
Db      760 ADEYVKGSGWGNNAFNNMLAS-----SHSYEYLHCFDTPYAPYIKNLTYIRQDSFEKG 814
Qy      815 SDGRGFSIGRLNLSPVQAKFYQDIDGSIYYDLSGFPVSDYRRNPOSTATLVMSPD 874
Db      815 TEGRSFDDSNLFTNLSPIVKFEKESDCNDFSYDLTSLVPPDLIRNDPCTTALVIGAS 874
Qy      875 WKIRGNLSROAFILRGSNVYNSNCELFGHYAMELRGSSRNINVDVGTURF 928
Db      875 WETVANNLARQALQVAGSHYAFSPWFVVLGQFVEVRGSSRYNADLGKRFQF 928

RESULT 10
US-10-289-762-470
; Sequence 470, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-470

Query Match      36.9%; Score 1763; DB 4; Length 930;
Best Local Similarity 41.7%; Pred. No. 1.2e-107;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

Qy      1 MKTSIPWVYVSSVYVFSCHLOSAN---BELSPDSDPFGNIDSGTFPPKTSAT---TTY 53
Db      1 MKIPLKLLISSTIVPI--LLSIATYGADASLSPDSDPFG--AGSITFTKSTADANGTY 58
Qy      54 SLTGDFVFEYEPGKGTPLSDSCFKQTTDNITFLGNHSLTFGFTDAGTHAGAASTTANKN 113
Db      59 VLSGNVYINDACKGTALTCCEFTETTGDLTFYKGYSFSGFNIVDAGSNAGAASSTADKA 118
Qy      114 LTFSGFSLSPDSPSTVTYTGQTLSSAGGVNLNIRKLVAAGNFST--DGAIKGA 170
Db      119 LFTGFSNLSFPAAPETVYASGKSTLSAGALNLTDNGLTILSÖVNSANANNNGAIIYAK 178
Qy      171 SFLTGTSGDALFSNNSSSTKGAIAITTAGARIANNTCYVAFSLNIASTSGAIDDEGTS 230
```

Db 179 TLISGTSITFTSNTSAKLGAIYSSAAASISGNTGQLVFNNMKNKGTGGALGFPASS 238
Qy 231 ILSNNKFLYFEGNAKTT---GGAICNTKASGPELIIISNNKTLIPASNVAETSGAIIHA 287
Db 239 SITONSSIFESGNTYTDAGKGAIIYCEKTEPILITISGNKSLTEPAENSSVITGGALICA 298
Qy 288 KKLALSSGGTFEFLRNNV-SSATPKGAISIDASGELSIAETGNITFVRNTLTGSTD 346
Db 299 HGLDLISAAGPTLFSNNRCNTAAGKGAIIADSGSLISANQDITFLGNTLTST-SAP 357
Qy 347 TPKRNAIINGNGFTELRAKNTIFFYDPTSEGT-SSDVLKINNAGALNPYQGTI 405
Db 358 TSTRNAIYLGSSAKITNLRAGGOSIYFPDIASTTGAISVLTINOPDSNPLDIYSGTI 417
Qy 406 LFSGETITADELKVAADNLKSSFTOPVSLSGKLLQKVLTLESTFSQEAISLLGMSGT 465
Db 418 VFSGKLSADBAKADNDFTSLIKQPLALASGTLALKGNVELDVNGFTQTEGSTLLMQPQT 477
Qy 466 TLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMF 525
Db 478 KLMKADTEAISLTKLVVDLSALEGNKSVSIEIAGANKTITLSPVQDSSGNFYESHITI- 536
Qy 526 HDQLFSL-LKITVDADVDTNVDISLLPVPADPNSEYGFQGGNNVMTTDTATNTEAT 584
Db 537 -NOAFTQPLVFTAAATAASDIYIDALLTSVPQTEPHYGOGHWEATW-ADTST-AKSGT 593
Qy 585 ATWTKTGVPSPERKALVNTLMGVFTDIRSLQOLVIEIGATGMEHKGFVWSMTNPLH 644
Db 594 MTWTTGTGNPERRASVVPDSLMASFTDIRLQOIMTSQANSIYQCGALMAGSTANFPH 653
Qy 645 KTGDENRKGFRHTSGGVYIGGSAHTPKDPLTFPAFCHLFARDKCFIAHNSRTYGGTLF 704
Db 654 KDKSGTQAFPHKSYGYIVGSAEDFSENIFSAFCQLFGKDKDLFIVENTSHNYLASLY 713
Qy 705 FKHSHTLOPQNYLRLGKAKFSESAIEKPREIPLADVQVFSHSDNRMETHYSLPSE 764
Db 714 LQHRAPFLG-----GLPMPSPGSIITDMLKDIPLILNAQLSYSTYKNDMDRRTSYPEAQ 766
Qy 765 GSWNECIAGIGIDLFPVLINPHLPFKTFIPQMKVEVAVVYVQNSFPFESSDGGFSGR 824
Db 767 GSWTNSGALBELGSLALYLPKEAPFFQGYFPFLKFOAVISRQOQFKESGAABAFDDGD 826
Qy 825 LNLNLSIPYGAFCVQDIDSYTYDLSGFFVSDVYRNNDPOSTATILVMSPDWKRIGNLSR 884
Db 827 LVNCSITPVGIRLEKISEDEKNNFEISLAVIGDVYKRNRSRSLVMSGASMTSLCKNLAR 886
Qy 885 QAFILRGSNNYVYNSNCELFGHYAMELFGSSRNIVVDGTLRF 928
Db 887 QAFILASGSHLTLSPHVELSGEAAVELRGSAMHIYVNDGCLRYSF 930

RESULT 11
US-10-312-273-45
; Sequence 45, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9

; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ. ID NOS: 664
; SOFTWARE: SeqWIn99, version 1.02
; SEQ. ID NO 45
; LENGTH: 930
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-45

Query Match 36.8%; Score 1761; DB 4; Length 930;
Best Local Similarity 41.7%; Pred. No. 1,7e-107;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

Qy 1 MKTISFVVLVSSVLASCHLOSLAN---BELSPDSFNGNIDSGFTFKTSA---TTY 53
Db 1 MKLPLKHLTSLTLVPI-LLSIATYGADASLSPDSFPG-AGSTFTPEKSTADANGTV 58
Qy 54 SLTGDVFEYEPGKGPLSDSCFKQTTDNLTFLGNHSLTFGFIAGTTHAGAASTTANN 113
Db 59 VLSGNVYINDAGKGTALTGCCFTETTGDLITFGKYSFSEFNTVDAGSNAGAASTADKA 118
Qy 114 LTFSGSLSDSSPSTVTTTGGTLLSSAGVNLNIRKLVAGNFSTA---DGAIKGA 170
Db 119 LFTFGSNISSFIAAPGTVASGKTLSSAGALNLTNGTLLFQONVSNBANNNGAITTK 178
Qy 171 SPLLITGSGALSNSSSTKGAIIATTAGARIANNQVYRPLSNLSTSGAIDDEGS 230
Db 179 TLISGTSITFTSNTSAKLGAIYSSAAASISGNTGQLVFNNMKNKGTGGALGFPASS 238
Qy 231 ILSNNKFLYFEGNAKTT---GGAICNTKASGPELIIISNNKTLIPASNVAETSGAIIHA 287
Db 239 SITONSSIFESGNTYTDAGKGAIIYCEKTEPILITISGNKSLTEPAENSSVITGGALICA 298
Qy 288 KKLALSSGGTFEFLRNNV-SSATPKGAISIDASGELSIAETGNITFVRNTLTGSTD 346
Db 299 HGLDLISAAGPTLFSNNRCNTAAGKGAIIADSGSLISANQDITFLGNTLTST-SAP 357
Qy 347 TPKRNAIINGNGFTELRAKNTIFFYDPTSEGT-SSDVLKINNAGALNPYQGTI 405
Db 358 TSTRNAIYLGSSAKITNLRAGGOSIYFPDIASTTGAISVLTINOPDSNPLDIYSGTI 417
Qy 406 LFSGETITADELKVAADNLKSSFTOPVSLSGKLLQKVLTLESTFSQEAISLLGMSGT 465
Db 418 VFSGKLSADBAKADNDFTSLIKQPLALASGTLALKGNVELDVNGFTQTEGSTLLMQPQT 477
Qy 466 TLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMF 525
Db 478 KLMKADTEAISLTKLVVDLSALEGNKSVSIEIAGANKTITLSPVQDSSGNFYESHITI- 536
Qy 526 HDQLFSL-LKITVDADVDTNVDISLLPVPADPNSEYGFQGGNNVMTTDTATNTEAT 584
Db 537 -NOAFTQPLVFTAAATAASDIYIDALLTSVPQTEPHYGOGHWEATW-ADTST-AKSGT 593
Qy 585 ATWTKTGVPSPERKALVNTLMGVFTDIRSLQOLVIEIGATGMEHKGFVWSMTNPLH 644
Db 594 MTWTTGTGNPERRASVVPDSLMASFTDIRLQOIMTSQANSIYQCGALMAGSTANFPH 653
Qy 645 KTGDENRKGFRHTSGGVYIGGSAHTPKDPLTFPAFCHLFARDKCFIAHNSRTYGGTLF 704
Db 654 KDKSGTQAFPHKSYGYIVGSAEDFSENIFSAFCQLFGKDKDLFIVENTSHNYLASLY 713
Qy 705 FKHSHTLOPQNYLRLGKAKFSESAIEKPREIPLADVQVFSHSDNRMETHYSLPSE 764
Db 714 LQHRAPFLG-----GLPMPSPGSIITDMLKDIPLILNAQLSYSTYKNDMDRRTSYPEAQ 766
Qy 765 GSWNECIAGIGIDLFPVLINPHLPFKTFIPQMKVEVAVVYVQNSFPFESSDGGFSGR 824
Db 767 GSWTNSGALBELGSLALYLPKEAPFFQGYFPFLKFOAVISRQOQFKESGAABAFDDGD 826

Qy 825 LNLNLSITPVKAKFPOVQGIIGSYTDGFGFVSVGVNNPNQSTATILMPSDSSKIRGKLTSLR 884
 Db 827 LVNCSIPIVGRILEKTSIEDCKNNPEISLAIIGVYKRNPRSRSTLSLVGASASTSTLCKTLAR 886
 Qy 885 QATLILGKSNNTYVNSNCELFPGHYAMELIRGSSNNYVNDVGTKLRF 928
 Db 887 QATLILAGSHLTLSIPVELLSGEAAALFKRSATITVYNDGCLKRSF 930

RESULT 12

```

Sequence 54680, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/256,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54680
LENGTH: 930
TYPE: PRF
ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54680

```

Query March	36.8%	Score 1761	DB 41	Length 930
Best Local Similarity	41.7%	Pred. No. 1.7e-107		
Matches 394	Conservative 165	Mismatches 355	Indels 30	Gaps 14
QY	1	MKTSIPMYLVSVLAFSCHLOSAN--EELISPDSPFNAGNIDSGFTTPKTSIA----	TTY	53
Db	1	MKIDLMKILISTVTPI-LTSLAVYGADASLSPDSDPDG--AGGSTTPPKSPADANGNINY		58
QY	54	SLTDDVFEEYBEGKGTPLSDSCFKQTDNULFTFGNSHSLTFPGIDGTAGAAASTYANKN		113
Db	59	VLSGNVYINDAGKGTALTGCCFETETGDLITFGKYSFSFNVVDAGSNAGAAASTTADKA		118
QY	114	LTFSGFSLTSDSSEFTTYYTGQGLTSSAGGVNLENIRKLVVAGNFSTH--DGAALICA		170

Db	119	L1PFGSLSLFLIACGTTIVASGKSTLSSAGALNTLDNGIILFSGNVSNMEANNNGAITTK	178
Qy	171	SPLLTGISGDLFENNSSSTKGAIATTAAGAIANNTRYVRLISNTASTBGGAIIDDEGTS	230
Db	179	TLISIGNTSITFTSNASKLGGAIYSSAMAISGWTGLVFNNNGETGGGALGFPASS	238
Qy	231	ILSNKKFLYFEGNAKTT--GGAICNTFASGSPELIISNNKFLIPASVNAETSGGAIHA	287
Db	239	SITQNSLFFSGNTATYTDAAKGGAICYCKETGETPILTITIGKNSLTTPAENSVTQGGAI	298
Qy	288	KKALSSGGTFEPLNNV-SSATPPKGAISIDASGELISAETGNTTFFVNTLITTTGSTD	346
Db	299	HGLDLSAAGPILFSNNRCGNTAAKGGAIAIADSGLSISANQDITFLGNTLTST-SAP	357
Qy	347	TPKRNAINIGNGKTELPAAKNHTIIPFDPTTSEGT-SSDYIKINNGSAGALNPYGTI	405
Db	358	TSTRNAIYLGSASKITNLRRAOGOSIYFYDPIASNTGTASDVLTINQPOSNSPLDYSGTI	417
Qy	406	LFSGGTLTFADELKVADNLKSFPTQPVLSGGKLLLOKQTLTLESTSPSOEAGSLGMOG	465
Db	418	VFSGEKLSADEKAKADNFTSILKQPLALASGTLALKGNVELDVNGTQTGTGSLTLNQPT	477
Qy	466	TLSTTAGSIITTNLGINVDSLGKQVSLTAKASNKVIVSGKLANLIDEGNIYESHMF	525
Db	478	KLKADTEAISTKLAVVDSLALGKNSVSJETAGANTITLTPSLVFDQSSGNGFYESH	536
Qy	526	HDQLFSL-LKTTVDADVDTNDISLIPVPADPNSEYFQOGOMNNWTTDTATNTKEAT	584
Db	537	-NOAFTQPLVVFATATAASDIYDALLTSPVGTPEBHYVYQGHWEATW-ADTST-AKSG	593
Qy	585	ATWTKTGVPSPERKSAVLCNTLMGVFTDIRSLQOLVEIGATGMEHKGQFWVSMTF	644
Db	594	MTWTTTGNPPEKASVVPDSLMASFTDIRLQOIMTSQANSIYQGRGMAAGTANFFH	653
Qy	645	KYTGDNKRGPHRTSGGYIVIGSSAHTPKDILFTFAFCHLPARDKCFIAHNSRTYGG	704
Db	654	KDKSGTNOAFPHKSGYIVIGSGAEDFSENIFFVAFCQLFGKDKDLFIVENTSHNYL	713
Qy	705	FKHSHTLOPQVYLRIGRAKFSESAIEKPPRELPLALDVQVSPSHNRMTHTSLP	764
Db	714	LQHAFLD-----GLPMPSTFGSITDMLKDIPLILNAQLSVYTXNDMDWTRTSLPE	766
Qy	765	GSWNECICAGGIGLDLPVLNSNPHLPKTFIQQMKVEMYVVSQNSFFESGSDRGFS	824
Db	767	GSWNNNSALBELGSLALYLPKEARFPQCYFFFLKFOAYNSQONKEGSAEARA	826
Qy	825	LNLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPOSTATLVMSPDSWKIR	884
Db	827	LVNCSIPVIGIRLEKISBEDEKNFFELISLAYIGVYRKNPSPRSITMWSGASWT	886
Qy	885	QAFLLRGSNNVYVNSCFLFGHYAMELRGSSNNVYDVDTKURF	928
Db	887	QAFLASAGSHLTLSPHVELSGEAAVELRGSAAIYVNDCLARSP	930

RESULT 13

```

US-10-289-762-472
: Sequence 472, Application US/10289762
: Publication No. US20040006218A1
:
: GENERAL INFORMATION:
:   APPLICANT: Grifflats, R.
:   TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
:   TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preven
:   TITLE OF INVENTION: and treatment of infection
:   FILE REFERENCE: 9710-003-999
:   CURRENT APPLICATION NUMBER: US/10/289,762
:   CURRENT FILING DATE: 2003-03-27
:   NUMBER OF SEQ ID NOS: 6849
:
:   SEQ ID NO 472
:     LENGTH: 927
:     TYPE: PR1
:
: ORGANISM: Chlamydia pneumoniae
:
: FEATURE:

```

NAME/KEY: SITE
LOCATION: 1...927
OTHER INFORMATION: Xaa=unknown or other
US-10-289-762-472

Query Match 36.8%; Score 1758.5; DB 4; Length 927;
Best Local Similarity 42.0%; Pred. No. 2,4e-107;
Matches 398; Conservative 153; Mismatches 357; Indels 39; Gaps 17;

```

QY 1 MKTSLPVLVSVYAFSGCHLO---SLANEELSPDDSPFNGNIDSGTFP-----TKSAT 51
DB 1 MKSSLHMFLLSSSLALPLSLNFSAPAAVEINLPGNPSFSG---PGYTPPAQTTNADGT 57
QY 52 TYSLTGVFEYEPKGPPLSDSCFKQTTDNLTLFGNGHSLTFEGFIDAGTHAGAASTTAN 111
DB 58 IYNLTGVSTINNASPTALTLASCKRETTGNLSFGHGQFLQIYIDAGANC-TTNTNAN 116
QY 112 KNLTFSGFSLSPDSSPSTVTTGQTLISAGVNLNIRKLVVAGNFTADGAIKAS 171
DB 117 KLSFSGFSYSLT--IOTTNATGTGAIKSTGACSIQSNVSCYFGQNFSDNGALQGS 174
QY 172 FLTLGTSGDALFSNNSSTKGAIATTAGARIANTGVRFSLNASTSGAIDDEGTSI 231
DB 175 ISLS-LNPNLTFAPKNKATQKQALYSTGCTITNTLNASAFSENTAANNGAIYTEASSF 233
QY 232 LSNKKFLYFEGN---AAKTGGAICNTKASGPELIISSNKKTLIFASNVAETSGAIIHA 287
DB 234 ISSKKAISFINNSVTATGATGAIYCSSTSAKPVLTISDGEINLTGNTAITSGAIIYT 293
QY 288 KKLAISSGGTFEPLRN--VSSATPKGAISIDASGEISLAETGNITFVNTLT--TGST 345
DB 294 DNLVYSSGGPTLFRKNSAIDTPAAPGGAIAIADSGEISLSALGDIPEEGNTVVKGAS 353
QY 346 DTPRNAINIG-SNCKFTELRAAKNHTFEYDPTISEGTS--SDVLKINNSAGALMPYQ 402
DB 354 QTTNNSININNTAKIVOLPASQGNITFYDPTITSTITALSDNLNPGDLGNAPAYQ 413
QY 403 GTILFSGEITLTADELKVNADNKSFTQPVLSGGKLLLOKGVLESTSFQSBAGSLIGMD 462
DB 414 GTIFSGEKLSEAEAEADNLSKTIQOBLTLAGGLSLKSGCVTLVAKSFQSPSTLMD 473
QY 463 SGTITSTTASITTTNLGINVDSIGLKQPVSLTAKGASNKYVSGKLNLDIEGNIYESH 522
DB 474 AGTTLLETDGSLSI--ICSQCFLEKRDQEXTLKATQAOQTTLTSGSLSLVPDGGVYEDV 531
QY 523 MFSHQFSLKITADADVNTNVDISLIPVAPEDPNSEYKPGOGMNWMTDPAATNKE 582
DB 532 SWNNQVFSCLTLT--ADDPANIHITDADPLEKNPIHWGVOGWAALSMQEDTRATSKA 589
QY 583 ATAATWTKGFVPSPERKALVNTLMGVFTDIRSLQOLVEIGATGMEHKOGFVWSSMTNF 642
DB 590 ATLWTTKGVNPNPERRGTIVANTLMGSPVDVRSIQOLVATKVRQSGCTRIGIWECEISNF 649
QY 643 LHKGTDENRKGPRHTSGGYVIGGSAHTPKDILFTFAFCHLPARDKDCFIANNSTRTYGT 702
DB 650 FHKDSTKINKGPRHSAGVVGATTTLASDNLITAAFCOLEKGDHFIKKNRASAYAA 709
QY 703 LEPKSHLQONVYRLGRAKSESAIEKPREITLADVOVSPFHSNNRMEHTHTLSPE 762
DB 710 LHLQHLATLSPSLRY--LPGES-----EQVULPDAQISYVSKNMTKTYTQAPK 760
QY 763 SEGSSNECIAGIGLIDLPVLSNPHPLFKTFIPOMKEMVNVVONSFPESSED--GRFSS 821
DB 761 GESSYNDGCALELASLPHRTALSHBGLFHAFFIKYKASITHODSKENTTLTVRFD 820
QY 822 IGRLLNLISIPVGAKEVQGDIGDSTYYDLSGFFVSDVYRNNPOSTATLVMSPDMSKIRGN 881
DB 821 SGDLINVSPIGITERFSRNERASYEAFVIYVADVYRKNPDCTALLINNTSMKTGTGN 880
QY 882 LSRQAFILRGSNVYVNSCELFHYAMELRRGSSNNVNDVGTCLRF 928
DB 881 LSRQAGIGRAGIFYAFSPLEVTLSNLSMEIRSSRSYNADLGKQPF 927

```

RESULT 14
US-09-452-380-3
Sequence 3, Application US/09452380
Patent No. US20020094340A1
GENERAL INFORMATION:
APPLICANT: WORDIN, Andrew D.
APPLICANT: OOMEN, Raymond P.
APPLICANT: MANG, Joe
APPLICANT: DUNN, Pamela
TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
TITLE OF INVENTION: US5 THEROP
FILE REFERENCE: 032931/0216
CURRENT APPLICATION NUMBER: US/09/452,380
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/132,272
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/113,439
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 936
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-452-380-3

Query Match 36.3%; Score 1734; DB 3; Length 936;

Best Local Similarity 39.9%; Pred. No. 1e-105;
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

```

QY 1 MKTSLPVLVSVYAFSGCHLOSLANEELSPDDSPFNGNIDSGTF-----TPKTSATYSL 55
DB 1 MKSSVSLFSSSILPFSLSISIVAAEVTLDSSNNSYDGS--NGTTFVFTSTDAAGTYSL 59
QY 56 TGVDFYFEPK--GTPLSDFCKQTTDNLTLFGNGHSLTFEFDIAGTHAGAASTT--ANKN 113
DB 60 LSDVSPFNAGALAIPLASGCFLEAGDITFGQOHALKFAPINAGSAGTVASTSAADKN 119
QY 114 LTFSGFSLSPDSSPSTVTT--TGQTLISAGVNLNIRKLVVAGNFTADGAIKGAASF 172
DB 120 LFRDFSRLLIISCPILLSPTQCALKSVGNLSLGNOSIITIQNPFSSNGGVINTKNF 179
QY 173 LTLGTSGDALFSNNSST--KGAIAATTAGARIANTGVRFSLNASTSGAIIDEGTS 230
DB 180 LLSGTSQFASFSRNQAFYTGKGGVYATGTTIENSPIVGSFQNLAKSGGALYSTDNC 239
QY 231 ILSNKKFLYFEGN---AAKTGGAICNTKASGPELIISSNKKTLIFASNVAETSGAIIH 286
DB 240 SITDNFQVIFPDGNSAMEAQAQGAICCTTTDKT--VTLGNKNLSFTNTTALTYGAIS 297
QY 287 AKKLALSGGTFEPLRNNSVATP---KGAISIDASGEISLAETGNITFVNTLTITTG 343
DB 298 GLKVISAGGPTLF--QSNISGSSHAGGCGGAIINASGELALHNTSDITF--NNQVING 355
QY 344 STDTPKRNAINIGNGKFTLRAAKNHTIFEYDPTISEGT--SSDVLKINNSAGALMPY 401
DB 356 STSR--RNAINIITDAVTSIRAAATGSIYFYDPTITPGRAASTDLNLMLADANSEIEY 413
QY 402 QGTLFSGEITLTADELKVNADNKSFTQPVLSGGKLLLOKGVLESTSFQSBAGSLIGM 461
DB 414 GGAIVFSGEKLSPKEKAIANVSTIRQPAVLARGDVLVDGVTVPFKDLTQSPGSLIM 473
QY 462 DSGTTLSTTASITTTNLGINVDSIGLKQPVSLTAKGASNKYVSGKLNLDIEGNIYES 521
DB 474 DGGTTLBAKEANLSLNLAVNLSDGTNKAALTEAADAOKISLSGTIALIDTBSGYEN 533
QY 522 HMFSDQLFSLKITVDADVNTNVDISLIPVAPEDPNSEYKPGOGMNWMTDPAATNTK 581
DB 534 HNLSASATYPLLETT--AGANGTITLGALSTLQEBETHYGVGNQLSMA--NATSSK 590
QY 582 EATWTWTKGFVPSPERKALVNTLMGVFTDIRSLQOLVEIGATGMEHKOGFVWSSMTN 641

```

Db 591 IGSINMTRTGYIIPSPERKSNLPLNSLWGNFIDIRISINQULIETKSSGEPFERELIMSGIAN 650
Qy 642 FLKKTGDENRKGFRHTSGGVYIGSAAHTPKDLETPAFCHLPARDKOCFLAHNNSRTYGG 701
Db 651 FFYRDSMPFRHGRHISGVALGITTATTPAEDQITPAFCQLFARDRHHITGKHGDTYGA 710
Qy 702 TLEFKHSHTL-OPONYLRUGRAKFSESAIEKPEPBEIPLADVQSFSDNRMETHYSL 760
Db 711 SLVFHHTBGLFDLANFL-WGKATRAPWVLSBISQIIPLSFDAKFSYLTHTDNHMKTYTDM 769
Qy 761 PSEBSGSNECTIAGIGLDLPVLSNPHLPKFTIPQMKVBYMYVQNSFFESSDGRGF 820
Db 770 SIIRGSWRNDARFADGASLPFVIVSVY-LIKEVEBFPVKQYIYAHQODFYERHABGRAP 828
Qy 821 SIGRLNLSIPVGAKEFVGDIQSDYDLSGFFSVDVYRNNPOSTATLVMSPDWKTIRG 880
Db 829 NKSSELINVELPIGVTFERDSKSEKGYDITLMTIYLRNPKQCQSLASDANMAAYGT 888
Qy 881 NLSRQAFLLRGSNNVYNSNCELFGHYAMELRGSSRNVDVGTCLRF 928
Db 889 NLARQGSVRAANHFOVNPHEIFGQFAFEVRSSSRNYTNLGSKCF 936

RESULT 15
US-10-324-129-3
; Sequence 3, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; NUMBER OF SEQ. ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO 3
; LENGTH: 936
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-10-324-129-3

Query Match 36.3%; Score 1734; DB 4; Length 936;
Best Local Similarity 39.9%; Pred. No. 1e-105;
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

Qy 1 MKTSPVVLVSVYLAFCCHLQSLANEELSPDDSFNGNIDSGTF-----TPKTSATTYSL 55
Db 1 MKSSVSWLFFSSSIDPLFSLSIVAEEVTLDBSSNNSYDGS-NGTTFVTSTTDAAAGTYSL 59
Qy 56 TGDVFEYEPK-GTPSLSDSCFKQTTDNLFLGNGHSLTFGFIADGTHAGAASTT-ANKN 113
Db 60 LSDVVSFQNAALGIPILASGCFLEKGGDLTFQGNQHALKFAFINAGSSAGTVAASTADKN 119
Qy 114 LTFSGFLLSFPDSSPTTVV-TGQGLTSSAGVNLLENIRKLVAAGNSTADGAIKASFP 172
Db 120 LTRNDFERLITICPSLILSPGQCALKSVGNLSLTGNSQIIFQNFSSDNGAGVINTKNF 179
Qy 173 LITGTSQDALFSNNSSTT-KGAIATTAAGARIANNNTGYRFLSNIASTSGAIDDEGTS 230
Db 180 LLSGTSQFASFSRNOATGKGQGVVATGTTIENSFGIVSFGONLAKSGGALYSTDNC 239
Qy 231 ILSNNKFLYFEGN---AAKTGGAICNTYASGSPILLISNNKTLIFASVVAETSGAIIH 286
Db 240 SITDNFQVIFDQNSAMEAAQAGGAICTTDTK--VTLGNKNKLSFTNTALTYYGGAIS 297
Qy 287 AKKLALSSGGFTETLRNNVSATP---KGAIISIDAGSELISAECNITFVAVNTLTTTG 343
Db 298 GLKVSISAGGPTTF-OSNIGSSAGGCGGAINIASAGELALSATSGDITF-NNNOVYTG 355

Qy 344 STDTPKRNAININGSKFTELRAAKNHTIFPYDPITSEGT--SSDVLKINNGSAGALNXP 401
Db 356 STST--RNAINIIDTAKTISIRAAQGSIFYVDPIITNPGTAASDTDLINLADANEIEY 413
Qy 402 QGTLIFSGETLRDELKADNLKSSFTQVSLSGGKLLIQKYTLTESTFSQAGALLGM 461
Db 414 GGAIVSGEKLSTEEKAIANYSTIRQPAVILARGDLVLRDGTIVFKDLTQSPGSRILM 473
Qy 462 DSGTSTTAGAGTTTNNLGINVDSGLKQPVSTAKGASNKVIVSGKLNLIIDEGNIYES 521
Db 474 DSGTTSAAENLISLGLVNLSSLDGTAKKALKTAAADKNLSLSTIALIDEGSFYEN 533
Qy 522 HMFSDQFSLKITVDADVDTNVDISSLIIPVAEPDENSEYGFQGGVNNWTTDTATNTX 581
Db 534 HNLKASATYPLLELT--AGANGTITLGALSTLTLQEPETHYGVQGMQLSMA--NATSSK 590
Qy 582 EATATYTKGFPPSPERKALVNTLWGVFTTIRSLQOLVEIGATGMEHKQGFVWSMTN 641
Db 591 IGSINMTRTGYIIPSPERKSNLPLNSLWGNFIDIRISINQULIETKSSGEPFERELIMSGIAN 650
Qy 642 FLKKTGDENRKGFRHTSGGVYIGSAAHTPKDLETPAFCHLPARDKOCFLAHNNSRTYGG 701
Db 651 FFYRDSMPFRHGRHISGVALGITTATTPAEDQITPAFCQLFARDRHHITGKHGDTYGA 710
Qy 702 TLEFKHSHTL-OPONYLRUGRAKFSESAIEKPEPBEIPLADVQSFSDNRMETHYSL 760
Db 711 SLVFHHTBGLFDLANFL-WGKATRAPWVLSBISQIIPLSFDAKFSYLTHTDNHMKTYTDM 769
Qy 761 PSEBSGSNECTIAGIGLDLPVLSNPHLPKFTIPQMKVBYMYVQNSFFESSDGRGF 820
Db 770 SIIRGSWRNDARFADGASLPFVIVSVY-LIKEVEBFPVKQYIYAHQODFYERHABGRAP 828
Qy 821 SIGRLNLSIPVGAKEFVGDIQSDYDLSGFFSVDVYRNNPOSTATLVMSPDWKTIRG 880
Db 829 NKSSELINVELPIGVTFERDSKSEKGYDITLMTIYLRNPKQCQSLASDANMAAYGT 888
Qy 881 NLSRQAFLLRGSNNVYNSNCELFGHYAMELRGSSRNVDVGTCLRF 928
Db 889 NLARQGSVRAANHFOVNPHEIFGQFAFEVRSSSRNYTNLGSKCF 936

Search completed: November 25, 2005, 14:29:58
Job time : 101.698 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:03:16 ; Search time 28.7195 Seconds
(without alignments)
2671.458 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 4782
Sequence: 1 MKTSLPWLVSVAFLSFCHL.....MELRGSSRNVDVGTGLRF 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5.COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6.COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H.COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCPUS.COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE.COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4782	100.0	967	2	US-09-438-185A-453 Sequence 453, App
2	4774	99.8	949	2	US-09-198-452A-478 Sequence 478, App
3	1855	38.8	928	2	US-09-428-122-2 Sequence 2, Appl1
4	1794	37.5	937	2	US-09-438-185A-449 Sequence 449, App
5	1763	36.9	930	2	US-09-198-452A-470 Sequence 470, App
6	1761	36.8	938	2	US-09-438-185A-448 Sequence 448, App
7	1758.5	36.8	927	2	US-09-198-452A-472 Sequence 472, App
8	1734	36.3	947	2	US-09-438-185A-447 Sequence 447, App
9	1593	33.3	780	2	US-09-438-185A-17 Sequence 17, Appl
10	1435.5	30.0	866	2	US-09-438-185A-15 Sequence 15, Appl
11	1355	28.3	932	2	US-09-438-185A-6 Sequence 6, Appl1
12	1345	28.1	922	2	US-09-198-452A-15 Sequence 15, Appl
13	1286	26.9	634	2	US-09-438-185A-451 Sequence 451, App
14	1286	26.9	643	2	US-09-198-452A-474 Sequence 474, App
15	1284.5	26.9	999	2	US-09-438-185A-455 Sequence 455, App
16	1278.5	26.7	973	2	US-09-430-723-2 Sequence 2, Appl1
17	1144.5	23.9	1414	2	US-09-438-185A-446 Sequence 446, App
18	1132.5	23.7	557	2	US-09-198-452A-29 Sequence 29, Appl
19	1130.5	23.6	671	2	US-09-198-452A-468 Sequence 468, App
20	1125.5	23.5	602	2	US-09-438-185A-18 Sequence 18, Appl
21	1092.5	22.8	1013	2	US-09-612-402B-15 Sequence 15, Appl
22	1092.5	22.8	1013	2	US-09-542-520-15 Sequence 15, Appl
23	1090	22.8	1012	2	US-09-612-402B-2 Sequence 2, Appl1
24	1090	22.8	1012	2	US-09-542-520-2 Sequence 2, Appl1
25	1089.5	22.8	1013	2	US-09-612-402B-16 Sequence 16, Appl
26	1089.5	22.8	1013	2	US-09-542-520-16 Sequence 16, Appl
27	1084.5	22.7	1006	2	US-09-556-877-190 Sequence 190, App

28	1084.5	22.7	1006	2	US-09-620-412C-190 Sequence 190, App
29	1084.5	22.7	1006	2	US-09-598-419-190 Sequence 190, App
30	1071	22.4	984	2	US-09-612-402B-43 Sequence 43, Appl
31	1069.5	22.4	982	2	US-09-556-877-176 Sequence 176, App
32	1069.5	22.4	982	2	US-09-620-412C-176 Sequence 176, App
33	1069.5	22.4	982	2	US-09-598-419-176 Sequence 176, App
34	1015.5	21.2	1132	2	US-09-198-452A-466 Sequence 466, App
35	995	20.8	507	2	US-09-198-452A-32 Sequence 32, Appl
36	850	17.8	880	2	US-09-556-877-175 Sequence 175, App
37	850	17.8	880	2	US-09-620-412C-175 Sequence 175, App
38	850	17.8	880	2	US-09-598-419-175 Sequence 175, App
39	843.5	17.6	494	2	US-09-198-452A-33 Sequence 33, Appl
40	843.5	17.6	497	2	US-09-438-185A-20 Sequence 20, Appl
41	839	17.5	866	2	US-09-556-877-189 Sequence 189, App
42	839	17.5	866	2	US-09-620-412C-189 Sequence 189, App
43	839	17.5	866	2	US-09-598-419-189 Sequence 189, App
44	831.5	17.4	427	2	US-09-198-452A-31 Sequence 31, Appl
45	827	17.3	483	2	US-09-198-452A-27 Sequence 27, Appl

ALIGNMENTS

```
RESULT 1
US-09-438-185A-453
; Sequence 453, Application US/09438185A
; Patent No. 6822071
;
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FaalSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0451
US-09-438-185A-453

Query Match      100.0%; Score 4782; DB 2; Length 967;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKTSLPWLVSVAFLSFCHLQSLANBELSPDSFNGNIDSGFTPKSATYSLTGDF 60
DB      40 MKTSLPWLVSVAFLSFCHLQSLANBELSPDSFNGNIDSGFTPKSATYSLTGDF 99
QY      61 FYEPKGTPSLSDSCFQQTNDLTFPLNGHSLTFGEIDACTHAGAAASTTANKNLTFSGFS 120
DB      100 FYEPKGTPSLSDSCFQQTNDLTFPLNGHSLTFGEIDACTHAGAAASTTANKNLTFSGFS 159
QY      121 LLSFSSPPTTYTTOGTLSSAGVNLNIRKLVAAGNSTDGDGAIKASFLTLTGTS 180
DB      160 LLSFSSPPTTYTTOGTLSSAGVNLNIRKLVAAGNSTDGDGAIKASFLTLTGTS 219
QY      181 ALFSNNSSSTKGAATATTAGARIANNQGYVRLSNIASTSGAIDDEGTSILSNKKFLYF 240
DB      220 ALFSNNSSSTKGAATATTAGARIANNQGYVRLSNIASTSGAIDDEGTSILSNKKFLYF 279
QY      241 ENNAKTTGGAICNTKASGSPLLIISNNKTLIFASVNAETSGAIIHAKKLAISSGGFTTF 300
```



```
Db 280 EGNAAKTTGGAICNTKASGSEPELLISNNKTLIFASNVAETSGAIIHAKKALALSSGGFTTF 339
Qy 301 LRNNVSATPKGGAISIDAGSELSLAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 360
Db 340 LRNNVSATPKGGAISIDAGSELSLAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 399
Qy 361 FTELRAAKNHTTFFYDPTITSEGTSDVLIKINNSAGALNPYQGTILFSGETTLTADELKVA 420
Db 400 FTELRAAKNHTTFFYDPTITSEGTSDVLIKINNSAGALNPYQGTILFSGETTLTADELKVA 459
Qy 421 DNKSSFTQPVSLSGSKLLQKGVLTSESTFSQEAAGSLGMDSGTTLTSTAAGSTITINLG 480
Db 460 DNKSSFTQPVSLSGSKLLQKGVLTSESTFSQEAAGSLGMDSGTTLTSTAAGSTITINLG 519
Qy 481 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
Db 520 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 579
Qy 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 600
Db 580 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 639
Qy 601 ALVNCNTLMGVFTDRLSLQOLVEIGATGMEHKQGFWSMNTNPLHKTGDENRKGFRTSGG 660
Db 640 ALVNCNTLMGVFTDRLSLQOLVEIGATGMEHKQGFWSMNTNPLHKTGDENRKGFRTSGG 699
Qy 661 YVIGSANTPKDIDFTFAFCHLPARDKOCFIAHNSNRTYGGTLFPKSHTLQPNYLRLG 720
Db 700 YVIGSANTPKDIDFTFAFCHLPARDKOCFIAHNSNRTYGGTLFPKSHTLQPNYLRLG 759
Qy 721 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 780
Db 760 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 819
Qy 781 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIGRLNLSTIPVGAKFVQGD 840
Db 820 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIGRLNLSTIPVGAKFVQGD 879
Qy 841 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDSWKIRGNI.SROAFLRGSNNYVYNSN 900
Db 880 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDSWKIRGNI.SROAFLRGSNNYVYNSN 939
Qy 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928
Db 940 CELFGHYAMELRGSSRNYNVDVGTCLRF 967

RESULT 2
US-09-198-452A-478
; Sequence 478, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 478
; LENGTH: 949
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; NAME/KEY: SITE
; LOCATION: 1...949
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-478

Query Match 99.8%; Score 4774; DB 2; Length 949;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 MKTISPMVLVSVLAESCHLOSLANEELSPDPSFNGNIDSGFTPEKTSATYSLTGDFV 60
Db 22 MKTISPMVLVSVLAESCHLOSLANEELSPDPSFNGNIDSGFTPEKTSATYSLTGDFV 81
Qy 61 FYEPGKGTPLSDSCFCQTTDNLTLFLNGHSLTGTGFIADGTHAANAATANKRLTFSGRS 120
Db 82 FYEPGKGTPLSDSCFCQTTDNLTLFLNGHSLTGTGFIADGTHAANAATANKRLTFSGRS 141
Qy 121 LLSFDSPTTLYTGGTSLSSAGVNLLENIRKLVNAGNSTADGAIKGSFLLTGTSGD 180
Db 142 LLSFDSPTTLYTGGTSLSSAGVNLLENIRKLVNAGNSTADGAIKGSFLLTGTSGD 201
Qy 181 ALFSNNSSSTKGGAITTAGARIANNTRYVFLSNIASTGGAIIDDEGTISLNNKFLYF 240
Db 202 ALFSNNSSSTKGGAITTAGARIANNTRYVFLSNIASTGGAIIDDEGTISLNNKFLYF 261
Qy 241 EGNAAKTTGGAICNTKASGSEPELLISNNKTLIFASNVAETSGAIIHAKKALALSSGGFTTF 300
Db 262 EGNAAKTTGGAICNTKASGSEPELLISNNKTLIFASNVAETSGAIIHAKKALALSSGGFTTF 321
Qy 301 LRNNVSATPKGGAISIDAGSELSLAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 360
Db 322 LRNNVSATPKGGAISIDAGSELSLAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 381
Qy 361 FTELRAAKNHTTFFYDPTITSEGTSDVLIKINNSAGALNPYQGTILFSGETTLTADELKVA 420
Db 382 FTELRAAKNHTTFFYDPTITSEGTSDVLIKINNSAGALNPYQGTILFSGETTLTADELKVA 441
Qy 421 DNKSSFTQPVSLSGSKLLQKGVLTSESTFSQEAAGSLGMDSGTTLTSTAAGSTITINLG 480
Db 442 DNKSSFTQPVSLSGSKLLQKGVLTSESTFSQEAAGSLGMDSGTTLTSTAAGSTITINLG 501
Qy 481 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
Db 502 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 561
Qy 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 600
Db 562 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 621
Qy 601 ALVNCNTLMGVFTDRLSLQOLVEIGATGMEHKQGFWSMNTNPLHKTGDENRKGFRTSGG 660
Db 622 ALVNCNTLMGVFTDRLSLQOLVEIGATGMEHKQGFWSMNTNPLHKTGDENRKGFRTSGG 681
Qy 661 YVIGSANTPKDIDFTFAFCHLPARDKOCFIAHNSNRTYGGTLFPKSHTLQPNYLRLG 720
Db 682 YVIGSANTPKDIDFTFAFCHLPARDKOCFIAHNSNRTYGGTLFPKSHTLQPNYLRLG 741
Qy 721 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 780
Db 742 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 801
Qy 781 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIGRLNLSTIPVGAKFVQGD 840
Db 802 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIGRLNLSTIPVGAKFVQGD 861
Qy 841 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDSWKIRGNI.SROAFLRGSNNYVYNSN 900
Db 862 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDSWKIRGNI.SROAFLRGSNNYVYNSN 921
Qy 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928
Db 922 CELFGHYAMELRGSSRNYNVDVGTCLRF 949

RESULT 3
US-09-428-122-2
; Sequence 2, Application US/09428122
; Patent No. 6872814
; GENERAL INFORMATION:
; APPLICANT: Comaught Laboratories Limited
; APPLICANT: Mordin et al.
```

TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
FILE REFERENCE: 19721-007-019
CURRENT APPLICATION NUMBER: US/09/428,122
EARLIER FILING DATE: 1999-10-27
EARLIER APPLICATION NUMBER: 60/106,046
EARLIER FILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/132,271
EARLIER FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 928
TYPE: PR
ORGANISM: Chlamydia pneumoniae
US-09-428-122-2

Query Match 38.8%; Score 1855; DB 2; Length 928;

Best Local Similarity 42.7%; Pred. No. 5,7e-131;
Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;

1 MKTSTPWWVSSVLAASCHLOSLANEELSPDPSFNGNIDSGFTFKTS---ATTYSLT 56
1 MKSSFPKPVSTPAIPP--LSMTATETVLDSSASPDGN-KNGNFVRESQEDAGTYLTK 57
57 GDFVFEY-PGKGTPLSDSCFKOTTDNLTFNGHSLTFGFIIDAGTAGA--STANKUL 114
58 GAVTLNIPOTGATIKSCFNNTKGDITFGNGNSLTFQVVDAGTYAAGAAVNSVVDKSI 117
115 TFSGFLSFDSSPSSTVTVTGQTL-SAGGVNLENIKRLVAGNFSTADGAIKASFL 173
118 TFIGFSLSPFIASPGSITTGKAVSCSTSLTKVNSLTFKNSFTDNGAITAKTULS 177
174 LTGTSGDALFSNNSSSTKGAIATTAGARIANNVYRFLSNASTSGAIDDEGSIIS 233
178 LTGTTSALFSESTSKGAIQTSALITTGQEVSEFSDNTSSDGAIFTEASVTLS 237
234 NKEFLV---EGNAKT---GGAI CNTKASGPELISNNKTLIFASVNAETSGA 284
238 NNAKVFIIDNKVTGASSSTTGDMSGAICAYKTSTDTKVTLTGOMLIPSNITSTAGCA 297
285 IHAUKLASGSGFTEFLRNVSAT-PKGAISIDASGELSIAETGNITFVNTLTG 343
298 IYVKUELASGGLTFRSNGVGTAPKGAIIEDSGELSLADSGDIYFLNVTYST- 356
344 STTPKRNAINISNGKFTFLRAKNHTTFYDPIT--SEGTSDVLKINSGALNPY 401
357 -TPTNRSSIDLTGSAKMTALRSAAGRAIFYDPITTGSETTYTDVLKVNETPADSALOY 415
402 OGTLFSGEFLTADDELKVADNLKSSFTQPVSLSGGKLLQGVLTSTSPSOEAGSLGW 461
416 TGNITTEGKLETEAADSKNLTSKLIQPVTLSSGTLISLHGVTLLQTOATQOADSLEW 475
462 DSGTTLSTAGSTITNGLINVSGLKQPVSLTAKASNKVLSGKLNLDIEGNIYES 521
476 DVGTGLE-PADTSTINNLVINISSIDGAKAKIETATSKNLTLSSGTTLLDPTGFYEN 534
522 HNSHDLSEFLKITYTADVDVNDISLLPVAEDPNSYEGOGQN-VNNTTDRANT 580
535 HSLRNPOSYDLELKASGTVTS---TAVPDPIMGEKFFYGOQWGPFWOTGASTT- 589
581 KEATATMTKTGFVSPERKALCNTLMGFTDIRISLQOLVEIGATMEKOGFWWSMT 640
590 --ATPNTKTGYIPNPRISLVPNSLMAFIIDISLHYMETANBEOQDRAFWCAGLS 647
641 NPLAKTGDENRKGRHSGGYVIGSANTPKDLPFPAFCHLPARDKCFIAHNSRTYG 700
648 NFPHKOSTKRRGRHLSGGYVIGCNLHTGSDKILSAFCQLPGRDRDYVVAKXGVV 707
701 GTLPFKSHSLQPNYRIKRAKFSESAIEKPREITLALDOVSPSHSNRKHETHTSL 760
708 GTLYYQHNET-----YISL-PCKLRPCSLSYVPEIPVLPFGNLSYTHNDNDKTKYTY 761

761 PSEGSWSNECIAGIGLDLPVLSPHPLFTFIIPQMKENVYVSQNSFFESSSDGRGF 820
762 PTVKSGWNGDSFALBFGRAPICL--DESALFQYMPFKLQVYAHQEGFKQTEARBF 820
821 SIGRLNLSIPVGAFF-VQGDIGDSTYDLSGFVPSDVYRNNPOSTATLVMSPDKIKG 879
821 GSSRLVNLALPIGIRFDEKSDQDA-TYNLTIGYVDLVRNSPDCCTYLIRISGDSWKTFG 879
880 GNLSROAFLLRGSNNVYVNSNCELFGHYAMELRGSSRRYNNVDVGTKLRF 928
880 TMLARQALVLRAGNHFCEFNSEAFSOFSELRGSSRRYNNVDLGAKYOF 928

RESULT 4

US-09-438-185A-449
Sequence 449, Application US/09438185A
Patent No. 6822071

GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue

APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 449
LENGTH: 937
TYPE: PR
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: CPr0447
US-09-438-185A-449

Query Match 37.5%; Score 1794; DB 2; Length 937;

Best Local Similarity 42.7%; Pred. No. 2.3e-126;
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

1 MKTSTPWWVSSVLAASCHLO---SLANEELSPDPSFNGNIDSGFTFP-----KTSAT 51
10 MKSSLHMFLLISSSLALPLSLNFSAPAAVEINLGFNPSFG--PETYPPAQTTNADGT 66
52 TSLTGDVFEYPPGKGTPLSDSCFKOTTDNLTFNGHSLTFGFIIDAGTAGA--STAN 111
67 TNLGCDVSTIAGASTYALTAFCFKETTNLSFOGHGYFLQNDIAGANC--TFNTAAN 125
112 KULTFSGFLSFDSSPSSTVTVTGQTLSSAGGVNLENIKRLVAGNFSTADGAIKAS 171
126 KULSFSGFYSL--IQTNATTGTCAIKSTGACSIQSVSCYFGQNFENDGALQOGSS 183
172 FLITGSGALFSNNSSSTKGAIATTAGARIANNVYRFLSNASTSGAIDDEGSI 231
184 ISLS--LNPULTRAKNAKATQKGAIVSTGITTNNLTNSASFENLTANNGALYTBASSF 242
232 LSNKFLVEEGN---AAKTGAI--CNTKASGPELISNNKTLIFASVNAETSGAIIA 287
243 ISNKAISFINNSVYATATSGAIIYCSSTSAPKPVTLSDNDELINIGTALTSGGAIYT 302
288 KULASGSGFTEFLRN--VSSATPKGAISIDASGELSIAETGNITFVNTLT--TGST 345
303 DNLVLSGSGPTLFXKNSAIDTAAPLGAIAIADSGSLISALGCIITFEAGNTVYKASSS 362
346 DTPKRNAINIG--SNKFTFLRAKNHTTFYDPITSEGS--SDVLKINSGAALNPYO 402
363 QTTNRSSINIGNNAKIVOLRASQGNITFYDPITTYSTIPLALSDALNLNPGDLAGNPAYQ 422

Qy	403	GTILFSEETLADLADKYADNKKSEFTOPVLSGGKLLKQKGVTEJSTFSFOEAGSLIGMD	462
Db	423	GTIFPSGKLSSEAEAEADNKKSTIOOPLTIAGQGLSKSGVTYLAASFQSGRSTLLMD	482
Qy	463	SGTTLSTTAGSITITNTLGINVDSLGLKOPVSLTKAGSNNKIVSGKLNLIIDIEGNIYESH	522
Db	483	AGTILEFTADG--ITINNVLANDVSLKETKKTLTKTQASQVUTLLSGSLSLDPSGNAVVEDV	541
Qy	523	MFSHDOLFSLIKTIIVDADVDVTNVDISLIPVAPADPASEXGFOGQMVNMTTPDATYTKE	582
Db	542	SNMNPQVPSCLTLT--ADDPANIHITDLADPLEKNPIHMGVQSNMALSNOEDTATSKA	599
Qy	583	ATAWTXTGVPVSPERSKALVCNTLWGVFTDIRSLQOLVEIGATGMEHKOGFWVSSMTNF	642
Db	600	ATLTWTKTGVYPNBERGCTLVANLTMGSEFVDVRSIOOLVATKVAQSOEETGIMWEGISNF	659
Qy	643	LHKTGDEMRKEFRHTSGGVYIGSAAHTPKDLPFACCHLPAPDKOEFIHNNSTRTGCT	702
Db	660	FHKOSTKKNKCFRHSAGVYVGATTTLASDULITAAFCQLFGKRDHFIKNRASAAYAS	719
Qy	703	LFFKXSHTLPONYLRLGRAKFSSEALKEPREIPLALDVQVSPSHSDNMEHTYSLPE	762
Db	720	LHLQHLATLSPSLTRY--LTPSES-----EQPVLPDAQISYIEKNTMKTYTTOAPK	770
Qy	763	SEGWSNECTIAGGIGLDLPFVLSNPHLPKFTFIQOMVEMYVQNSPEFESSD--GGGFS	821
Db	771	GESSWYNDGCALIELASSLPHLTALSHEGLEFAHYFFPIKEASYIHQDSFKENNTLVLSFD	830
Qy	822	IGRLNLNLSIPGAKFVQGDIGDSTYYDLSGPFVDVYRNNQOSTATYLVMSBDSWKIGCN	881
Db	831	SGDLINVSVPIGITPERSRNERASYEATVIYADVVRKNDPCTTALLINNSTKTTGTN	890
Qy	882	LSRQAFLLRGSNNYVYNSNCELFQHYAMELALGSSRNYYVGYTKLRF	928
Db	891	LSRQAGIGRAGI FYAFSPNLEVTNLSMEIGSSRSYVADYAGKFFQF	937

```

RESULT 5
US-09-198-452A-470
; Sequence 470. Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflab, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments,
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198.452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-470

Query Match          36.9%: Score 1763; DB 2; Length 930;
Best Local Similarity 41.7%: Pred. No. 4,9e-124;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

QY      1 MKTSPWLVSSVAFSCHLOSAN--EELISPDSFENGINDSGFTTPKTSA----TTY 53
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1 WKIPHLKLISSTLVTPI-LLSIATYGDASISPFDSFDG-AGSTFPFKSTADANGNTY 58
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      54 SLTGVVFFPEPECKGTPPLSDSCFKQTTDNLPLGNHSLTLPGLDGTAGAGAASTTANKN 113
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      59 VLSGVVYINDAKGKALTGCCPTEFTTGBLTFGKGYSPSFNTVDGNSAAGAASTTADKA 118
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      114 LTFSGEFLSPDSDPTVTTGQGLSSAGVNLNIRKLVAAGNFTA--DGAIRGA 170
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      119 LTFTFPSNLSFIAAGCTTVASGKSTLSSAGALNLINDNGTILFQSVVNSBEANNNGAIIYAK 178
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      171 SFLTGTSGDALFSNNSSSTYKGAIIATTAGARIANNGTGVREPLNSIASTSGAIDDEGTS 230
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Dd	179	TLTISGNTSSITFTFNSNAKKUGALYSSAASISGNTQVLFPNNKGETGGALPFBAB	238
OY	231	ILSNKKFLYFEGNAAKTT--GGAICNTKASGSPILLISNNKTLIPASVNETSGALITHA	287
Dd	239	SITONSISFFPGNATYDAAGKGAICYCBKGETPILLISGNKSLFPAENBSYUQGAICA	298
OY	288	KKLAISSGCFEPLRNNV--SSATPKGASISIDAGSELBSAETGITEVNRNLTITGSTD	346
Dd	299	HGLDLSAAGPLTFNNRCGNTAAGGAGALADSGSLBSANQGITFLGNLTST-SAP	357
OY	347	TPKRNAINIGSNGKFTBLPAAKNHTIFPYDPTSEGT--SDVLYKINNSAGALNPYQGTI	405
Dd	358	TSTNRNAYLIGSSAKITMNRRAOGOSIPEYDPJASMTTASDVLTNOPDSNPLDYSGTI	417
OY	406	LFSGEITLADDELKADNLSKSPFQVBSJSGGLTLQKQVTESTSFSGEAGSLGMDSGT	465
Dd	418	VFSGKLSADEKKAADNFTSLIKQPLALASGLTALKGVNDELVDNGFTQEGSTLMDPBT	477
OY	466	TLSTTAGSITITNGLINVDLSGLKQVSLTKGASNKYIVSGKLNLDIEGNIYESHMS	525
Dd	478	KLKADTEAISLTKLVVDLSALEGNKSVSIEFTAGAKTITLTSPLVFQDSGNFYESHIT-	536
OY	526	HDQLFSL-LKITTVDADVTDNDISLIEVPADPNSEKGFQCGQNNVNTTDPATNTKENT	584
Dd	537	-NOAFTQPLVFTATATAASDIYIDLTLTSVPQTPPHYGOQHMWATV-ADTST-AKSGT	593
OY	585	ATWTKTGVPSPERSKALVNTLMQVFPNDIRSLQOLVEIGATGMEHKOGFVWSMTNPLH	644
Dd	594	MTWTTGTGNPDERBASVVPDSLMASTFDIRTLQOIMTSQANSITVOQRILMASGTANPFH	653
OY	645	KTGDENRKGFRTHTSGGYIVIGSSAHTPKODLFTFAFCHLPARDKOCFIAHNSRTYGGTLP	704
Dd	654	KDKSGTNOAFPRKRSYGYIVGSGAEPSEENIFEVAFCOLFGKPKODLFIVENTSHNYLASY	713
OY	705	EKHSITLQPOYVLRGKAFSESALIEKPRELPIALDVQVSSHNDNREHTYSLPESE	764
Dd	714	LOHRAFLLG-----GLPMPSFGSTITMDKIDPLILNLOLSTSYTNDMDTDITYSLPEAQ	766
OY	765	GSMNSNECIAGGIGLDLPEVLNSPHPLFTFIPIQMKEVEMYVVSQNSFPRESSDGRGFSIGR	824
Dd	767	GSMTNNSGALBELGSLALYLPKEAFPFQGYPPFLKFOAYYSHQONFKESGAELARADDG	826
OY	825	LINTSIPYGAKFVQGDIGDSYTYDLSGFVSDVYTRNNPOSTATLYMSPDMSKIRGNLSR	884
Dd	827	LYNCSIPYGIRLEKISEDEKNNFEISLAYIGVYKRNPSRSTLWVSAGASWTSJLCKNLAR	886
OY	885	CAFLRGSNNYYNNCLEFGHYAMELRGSSNNYVNDVCTKURF	928
Dd	887	QAFLLASAGSHLTLSFHVLSLGEAAIELRSSAIIIVNDCGLRYSF	930

```

/ RESULT 6
/ US-09-438-185A-448
/ Sequence 448, Application US/09438185A
/ Patent No. 6822071
/ GENERAL INFORMATION:
/ APPLICANT: Stephens, Richard
/ APPLICANT: Mitchell, Wayne
/ APPLICANT: Kalman, Sue
/ APPLICANT: Davis, Ronald
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
/ FILE REFERENCE: 018941-000411US
/ CURRENT APPLICATION NUMBER: US/09/438,185A
/ CURRENT FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: US 60/108,279
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: US 60/128,606
/ PRIOR FILING DATE: 1999-04-08
/ NUMBER OF SEQ ID NOS: 1074
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 448

```


QY 643 LHKTGDNBRKGFRTSGGVYIGSAHTPKDDLFTFAFCHLPARDKOCFIANNHNSRTYGGT 702
 DB 650 FHKSTINKCFRISIGYVVGATTTLASDNLITAAICQLFGKRDFINKNRASAAYAS 709
 QY 703 LFFGHSHTLQOPNYLRIGRAFSESALKEFPREIPLALDVQVFSHSDNMETHYTSLPE 762
 DB 710 LHHGLMTLSSPILRY--LPGSES-----EQVLPFDAQISYISKMTKTYTQAPK 760
 QY 763 SEGWSNECIAAGGIGLDLPFLSNPHLPFKFTIPQMKVEMYVQNSFFESSSD-GRGFS 821
 DB 761 GESSWYNDGCLLELASSLPHTALHEGLFHAFFPPIVEASYIHQDSFKENNTLVASF 820
 QY 822 IGRLLNLSIPYAKFVQGDIGSYTYDLSGFFVSADVYRNNPOSTATLWSPDSWKIRGN 881
 DB 821 SGDLINVSPIGFTIFPERSRNRERASYEATYVADVYRKAPDCTTALLINNTSKTGTN 880
 QY 882 LSRQAFLLRGSNNYVNSNCELFGHYAMELRGSSRNYNVDVTKLRF 928
 DB 881 LSRQAGIGRAGIFYAFSPNLEVTSLNLSMEIRGSSRSRYADLGKFOF 927

RESULT 8
 US-09-438-185A-447
 / Sequence 447, Application US/09438185A
 / Patent No. 6822071
 / GENERAL INFORMATION:
 / APPLICANT: Stephens, Richard
 / APPLICANT: Mitchell, Wayne
 / APPLICANT: Kaiman, Sue
 / APPLICANT: Davis, Ronald
 / APPLICANT: The Regents of the University of California
 / TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
 / FILE REFERENCE: 018941-000411US
 / CURRENT APPLICATION NUMBER: US/09/438,185A
 / PRIOR FILING DATE: 2002-03-13
 / PRIOR APPLICATION NUMBER: US 60/108,279
 / PRIOR FILING DATE: 1998-11-12
 / PRIOR APPLICATION NUMBER: US 60/128,606
 / PRIOR FILING DATE: 1999-04-08
 / NUMBER OF SEQ ID NOS: 1074
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 447
 / LENGTH: 947
 / TYPE: PRT
 / ORGANISM: Chlamydia pneumoniae
 / FEATURE:
 / OTHER INFORMATION: CPn0445
 / US-09-438-185A-447

Query Match 36.3% Score 1734; DB 2; Length 947;
 Best Local Similarity 39.9%; Pred. No. 7.7e-122; Indels 32; Gaps 18;
 Matches 378; Conservative 182; Mismatches 356;
 QY 1 MKTSLPWLVSVALFSCHLQSLANEELSPDSENGNIDSGTF-----TPKTSATYSL 55
 DB 12 MKSSSWLFFESSILPFFSSLSIVAALVTLDSSNNSTDGS-NGTTFVFSTDDAAAGTYSL 70
 QY 56 TGDVFFYEBGK-GTPUSDSCEFKQTDNLTLFLNGHSLTFGFDAGTAGAAAST-ANKN 113
 DB 71 LSDVFFONAGALGIPLASGCFLEAGGDLTFQGNQHALKFAFNAAGSSAGTYASTAADKN 130
 QY 114 LTFESGSLSPDSSPTVT-TGOGTILSAGGVNLENIRKLVVAQNSFTADGAIKGASF 172
 DB 131 LTFNPSRLSTISCSPLSLPTGQCALKSVGNLSLTGNSQITFTQNFSSDNGVINTKNF 190
 QY 173 ILTGTSGDALFSSNSSST--KCGAIAATTAGARIANNYGVRLSNIASTSGAIDDEGTS 230
 DB 191 LLSGTISQFSPFRNQAFTKQGGVYATGTITIBNSPGIVSPSQMLAKSGGALYSTNDC 250
 QY 231 ILSNKKFLYEGN---AAKTGGAICNTKASGSPELLIIISNNKTLIFSNVAETSGAIIH 286
 DB 251 SITDNFOVIFDGNASMEAQAOGGAICTTTDKT--VTLTGKNLSTFTNTALTYYGAIS 308

QY 287 AKKALSSGGFTFELRNNSATP---KGAISIDASGELSASATONITFVRNLTITG 343
 DB 309 GLKVISIAGPPLTF-QSNISGSSAGGGGALINIASAGELASATNSDITF--NNQVING 366
 QY 344 STDTPKRNAININGSKFTELPAKKNTIFFYDPTISEET--SDVLKKNNSAGALNY 401
 DB 367 STET--RNAIINIDTAKVISIRAAQOSIYFPDPTINPGTAASDTLNLNLANDANSEIEY 424
 QY 402 OGNTLPSGFTLPADELKVDNLSKSFQPSVSGGKLLQKQVLTSETSFSQDAGSLQM 461
 DB 425 GCAIVSSEKLTSTKALIANVTSTRQPAVLARGDLVARDVYTFKQLTQSPGRIIM 484
 QY 462 DSGTTLSTAGSITITNLGINVDSIGLKOPVSLTAKGANKYVSGKLNLDIEGNIYS 521
 DB 485 DGGTTLISAKVANLSLGLAVNLSLDGTAKKALKTEAADKNISLSGTIALIDTEGSPYEN 544
 QY 522 HNSHQULSLLKITVDADVOTVDSLSLIPAEAPNBEYFGQGMNVMNTDPTATNPK 581
 DB 545 HNKSASTYPLBELTT-AGANGTITLGAALSTLLOEPETHYGYQGMQLSMA--NATSK 601
 QY 582 EATATWTKTGFVSPERKSALVCNTLGVFTDIRSLQQLVEIGATGMEHKOGFVWSMTN 641
 DB 602 IGSINWTRTGYLSPERKSNLPLNSLNGNFIIDRSINOLIFTKSSGEPFERELMISGIAN 661
 QY 642 FLHKTGDNBRKGFRTSGGVYIGSAHTPKDDLFTFAFCHLPARDKOCFIANNHNSRTYGG 701
 DB 662 FFYRDSWPTRHGFRHISGGYALGITATTPAEDQLTFAFCQLFARDRHHITGKNHGDYGA 721
 QY 702 TLFPHKSHTL-QOPNYLRIGRAFSESALKEFPREIPLALDVQVFSHSDNMETHYTSL 760
 DB 722 SLVFHHTGEGFDIANPL-WKATRAPVAVLSEISQILPLSDAKFESLHTDNHAKITYTDN 780
 QY 761 PESEGSWSNECIAAGGIGLDLPFLSNPHLPFKFTIPQMKVEMYVQNSFFESSSDGRGP 820
 DB 781 SIITKGRNDAPCADLGAISLPYISVPY-LKKEVEFVAVQYIYAHQGFYEHAAGRAF 839
 QY 821 SIGRLNLSIPYAKFVQGDIGSYTYDLSGFFVSADVYRNNPOSTATLWSPDSWKIRG 880
 DB 840 NKSELINVEIPIGVTFERDSKSEKGYDILMYITLDAYRRNPQCQSLIASDANMAAYGT 899
 QY 881 NLSROAFLLRGSNNYVNSNCELFGHYAMELRGSSRNYNVDVTKLRF 928
 DB 900 NLRQGFVRAAHFQVNPMEIFGQFAFEVRSSSRNNTNLSKRCF 947

RESULT 9
 US-09-438-185A-17
 / Sequence 17, Application US/09438185A
 / Patent No. 6822071
 / GENERAL INFORMATION:
 / APPLICANT: Stephens, Richard
 / APPLICANT: Mitchell, Wayne
 / APPLICANT: Kaiman, Sue
 / APPLICANT: Davis, Ronald
 / APPLICANT: The Regents of the University of California
 / TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
 / FILE REFERENCE: 018941-000411US
 / CURRENT APPLICATION NUMBER: US/09/438,185A
 / PRIOR FILING DATE: 2002-03-13
 / PRIOR APPLICATION NUMBER: US 60/108,279
 / PRIOR FILING DATE: 1998-11-12
 / PRIOR APPLICATION NUMBER: US 60/128,606
 / PRIOR FILING DATE: 1999-04-08
 / NUMBER OF SEQ ID NOS: 1074
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 17
 / LENGTH: 780
 / TYPE: PRT
 / ORGANISM: Chlamydia pneumoniae
 / FEATURE:
 / OTHER INFORMATION: CPn0015
 / US-09-438-185A-17

Query Match	30.0%;	Score 1435.5;	DB 2;	Length 866;
Best Local Similarity	-35.9%;	Pred. No. 2.1e-99;		
Matches 340;	Conservative 147;	Mismatches 335;	Indels 125;	Gaps 15;

```
QY      1 MKTSLPWLVSVAFS-CHQLSANELLSPDPSFNGNIDSGCFTEPKTS-----TTYSL 55
Db      26 MKLPLRFLISLVYTLMSNLGATTEBEJSASNPFGITSTISSFKTSATSATGTINYV 85
QY      56 TGDVPFYFE-GCKGPPLSDSCFKQ--TTDNLTFLONGHSLTFGEFDAGTHAGA-A-STTAN 111
Db      86 KDSVLIENVPRTGSTGTSTCFKNDAAAGDLNFLGGGRSFPTSNIDATTAAGSAIGSEBAN 145
QY      112 KNULTFSGEFLSPDSSPSTVTYTTCGGTLLSAGVNLNIRKLVANGFTADGAALIKAS 171
Db      146 KTVLISGFSAISFLKSPASTVTNLGAINVKGNLSLDNRKVLIQDNFSTDDGCAINCAG 205
QY      172 FLTGTSGDALFSNNSSSTKGAIATAATTAGARIANTGVYVFLSIASFSGAIDDEGSI 231
Db      206 ----- 205
QY      232 LSNKKFLYFEGNAAKTTGCAICTKAGSGPELLISNNKTILFAFNVAETSOGAIHANAKLA 291
Db      206 -----SLKIANNKSLSFIENSSSTRGAIHTKNLT 235
QY      292 LSSGFTPELRNNVSATPYKGAISIDAGELSLSAETGNITFYVRNTLTTTGSTDPTRKN 351
Db      236 LSSGFTLFQONTAPTPAAGKGAIAIADSGTLSISGSDGIIFEGNTI---GATGVSHS 292
QY      352 AININGSKFTELPAANKHTFFPDAPTSEBTS--DYLNKINSAGALNRYOCTILFSG 409
Db      293 AIDGTSAKTALPAAGKITYPFDPIYVGSTSAAALNINSDDTGDKNEYTGIVYFG 352
QY      410 ETLPADELKYADVNLKCSFTOPVSLSGKLLLOKCVLTLESTSFQESGLMDGDTTYLT 469
Db      353 EKLTBAKDEKARTSKLQNVAKRGNTVLKGVULSANGFSDANSKLMIDGTSIVA 412
QY      470 TAGSITTNLGINVDSLGLQPVSLAKGASNKVIYSGLNLDIEGNIYESHMFSDOL 529
Db      413 NTESIELTNLEINIDLPRNGKKIKLSAATAOKDIRIDRPVVLAIDSDFYNGELINEDHS 472
QY      530 F-SLLKTTVDADVTDNVDISLFIYVPADPRSSEYFGQGMVNMTTDTATTKATATWT 588
Db      473 YDGLIELDACKDVIYASDRSIDV----QSPGYGQAKTIWNSTD--DKATYSWA 523
QY      589 KTGVSPSPERSALVCNTLWGCVFTDIRSLOOLVEIGATGMEHKGFPMWSMWNFLAHKTGD 648
Db      524 KQSNLPFADEGARPLVPMLLMGSFIDVASFQNFILGTREGARPERGRFVYAVAGISNVLIHSGR 583
QY      649 ENRKGFPHRTSGGVYIGGSAMTPKODLTFFAFCHLPADKOCFIANNRSITYGTLFPGRHS 708
Db      584 ENQGKFPHVSGAVAGVASTMPGDDTSLGFAQLFADKDXFYMNNTNPAKTYAGSILRLQHD 643
QY      709 HTLOPQVYLUGRAKKBESAIEKRPRRIPLALDVQVESHSDNMETHYSLP----- 761
Db      644 ASLSVSVALGEGGLREILLPYVSKTLPGCFYGQALSYGHTDHMKKE--SLPPPTPLS 701
```

[illegible]

RESULT 11
US-09-438-185A-6

```

Sequence 6, Application US/09438185A
Patent No. 6822071
GENERAL INFORMATION:
APPLICANT: Stephen, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kaiman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 932
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: CPh0005
US-09-438-185A-6

```

Query Match 28.3%; Score 1355; DB 2; Length 932;

Best Local Similarity 35.4%; Pred. No. 2.7e-93;
Matches 339; Conservative 155; Mismatches 399; Indels 64; Gaps 21;

3 TSIPWLVSSVLAFSCHLOSLANEEL-----LSPDDSFNGNIDSGTFPIPKTSA-FTYSL 55

9 TKMRFSLGCPPLVFSFTLLSVFDTSLSATTISLTPEDSFHGDSSQNAERSYNYQAGDYSL 68

56 TGDVFFYEPRGKSTPLSDSCFKQTDDNLFLGNHSLTFGFI DAGTHAGAAASTTANKNLT 115

69 TGDVSTSNV-DNSALNKACFNTVSSGTYFAGNHGGLYFNNISSGTTKEGAVLCCQDPQAT 127

116 --FSGFSLSFDSPTVTITGGTSLSAGVNLNIRKLVAAGNFSTADGAIKGSFL 173

128 ARSGFSTLSIQPGD--IKEQGLYKNALMLNNYVRFEEQNSKTKGSAISGNVT 185

174 LTGTSGLAFSNSSSTKGAIAATTAGARIANNYGVRFSLNIAS*--GGAIIDDEGTSIL 232

```

186 IVGVYDSVSEFYQN-AATFGCAIHSSGPLQIAVNGAEIRFAQNTAKNGSGGALYSDGDIDI 244

```

233 SNNKFLYFEGNAKTT---GGAICNTRKASGS---PELIISNNKTLIPASNVAEISGA 284

245 DQNAVYLFRENEALTTAIGKGVCCUPTSGSSTPVPIVTFSDNQLVFERHNSIMGGA 304

285 IHAKLALSSGGFTEFLRNVSATPK--GGAISIDASGELSUAETGNTTFVRNTLTIT 342

305 IYARKLSISSGGPTLFI -NNISYANSQNLGALADTGGELISLSAEKGTITFGQN ----- 358

343 GSTDTPKRNAINIGSGKFTELRAAKNHTIFFYDPITSEGTSSDVLKINNGSAGALNPYQ 402

359 -RTSLPFLNGIHLLQNAKFLKLQARNGSIEFYDPTITSEADSTQLNINQDPKN--KEYT 415

```

QY      403 GTILFSGGTLTVADEKLVADNKLKNSFTQVSLSSGGKLLLOKQVTLTSTSPSSQAGSLILMD 462
Db      416 GTILFSGKSLANDR---DFKSTIRQVNVLSAGVLVKEGAEVYVSKRTQSGPBGHLYVD 472
QY      463 SGTLLSTTAGSITTTNNLGINVDLSGLKQPVSLTAKGASNKVY-VGGKLNLDIEGNIYSS 521
Db      473 LGTKLAKEDIALITGLAIDIDSLSSSSSTAAYIKANTANKOISTVDSIELISPTGAUYED 532
QY      522 HMFHSDOFLSLKITVDADVDTNNVDISLIPVAPADPNSEYFQOGOMVNMVMTTDATATNK 581
Db      533 LMRMSQFFPLLSLEPAGCAGSVTYAAGFLPV-----SPHYFGQGNWKLA---IGTGAK 584
QY      582 EATATWTTGTGEVPSPERKSALVCTNLWGFYFDIRSLQOLVEIGATGMENHKQGFWYSSMTN 641
Db      585 VGEEFWDKINKKPREKEKGNLVPLNIMGNAVDYRSLIMOQOEHAASLQTDREGLIMDIGEN 644
QY      642 FLHKGTGDNRRKGFRHTSGGVYTG-GSATPRKDLFTPAFCHLFAADKCFIAHNSRTYG 700
Db      645 FFHVASADNIRYRINSSGGYULSVNNELTPK-HYISMAFSQLFSDKDYAVANNEMRWLY 703
QY      701 GTLFPEKHSHTL-----OPONYLRLGRAKESSEALIEKPREIRPLALDVQVSPESHSDN 751
Db      704 GSLYLQVTTSLGNIIPRYASRNPNVAVUGILSRFLQNP.L-----MTRPFLCAYOHANT 755
QY      752 RMETHYITSLPBEGSWSNECTAGAGIGLDLPVLSMNPRLFKTTFPOMKEMVYVSSONSFF 811
Db      756 DMKIDYANFPMVKNSWRNNCWAIECGGSGRPLLVFENGRLFLQALIRPMKIQLYVAYGDPK 815
QY      812 ESSSDGRFSGISGRLLNLSIPVGAKEPVQGDIGDSTYYDLSGEFVSDVYRNNPOSTATLVMS 871
Db      816 ETADAGRFRFNSGSLNISIVPLGIRREKALISQDVLVDFSFYSIPIDFIRDPCEALAVIS 875
QY      872 PDSWKIRGNLSRQAFLLRGSNNYYNNSCELFGHYAMELRRSSSRNNYNDVGTIKLRF 928
Db      876 GDSWLVPAHAYSRHAFVSGGTGRHYHFNDDTELLCGSIECRPHARYNINQCSKEPF 932

```

RESULT 12
US-09-198-452A-15
; Sequence 15, Application US/09198452A

```

; Patent No. 6559294
;
; GENERAL INFORMATION:
;
; APPLICANT: Griffais, R.
;
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
;
; TITLE OF INVENTION: and treatment of infection

```

```

; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
;

```

```

; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

```

```

; SEQ ID NO 15
; LENGTH: 922

```

```

;
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
;

```

```

; FEATURE:
; NAME/KEY: SITE
;

```

```

; LOCATION: 1...922
; OTHER INFORMATION: Xaa=unknown or other
;

```

US-09-198-452A-15

	Query Match	Best Local Similarity
28.1% Score 1345; DB 2; Length 922;	35.4% Pred. No. 1.5e-92;	

Matches	335;	conservative	154;	mismatches	353;	indels	64;	gaps	21.
---------	------	--------------	------	------------	------	--------	-----	------	-----

0Y
14 LAFSCHLOSANNEEL-----LSEUDSFNGNLSGIFRNIISA*11ISLSVDVFIEFGA 06

DB 10 LWFSEILSVHDISLSTIISLIEFDSFHGDSQNAEKSINVQAGDVISLSDVSSISNV-D 08

```
67 GIPUSDSCFQITDNLIFEGNGSHLFFGFIDAGIHAGAAAS IANNKLI --FSGFSLSLF 124
```

69 NSALKKACFXYISGSVIFAGNHGAYFINNIBSGIKSGAVLCCYDFQAIARFSGFIASF 120

QY 125 DSSPSITVITIGGGILSSAGGVNLENIRKLVAAGNFSIAUGGALNGASFLLIGISGDAUFS 184

Db 129 NOSFGD--1KEQGCLYXKAMLMHLLNYYVREFQNSKTKGAIISGANTVIYGNDSIFY 166

Qy 185 NNSSTYKGAIAATTAGARIANNTGYVRLSNIAT--SGCAIDDEGTSILSNKKELYEFGN 243

Db 187 QN-AAFGGAIHSSGPIQLAVNQAEIRFAQNTAKNGSGGALVSDDDIDIDQNAVYLRFN 245

Qy 244 AAKTT-----GGAICNTKAGS----PELLISNNKTLIPASVALETSGGAIHAKKLALSSG 2295

Db 246 EALTTLTGKGAIVCCLPITSGSSTPVPVLPFSNNKQLVFERHNSIMGGAIAARKLSISG 3053

Qy 296 GTFEPFLRNVSATPK--GGAISIDPAGSLSAETGNITFPBRLTLTGTSTDPKXNAI 3535

Db 306 GPLLFT--NNISYANSQNLGGAIALDTGGISLSAKGITTQGN-----RTSLPLNGI 3568

Qy 354 NISNGKFTELRAAKNHTIFPYDPITSEGTSSDVLLKINNGSAGALNPYGTILFSGEILT 4133

Db 359 HLLQNAKFKLQLQNRNGYISIEFYDPTISEADGSTQLTNINGDPKN--KEYTGLTILFSGKSL 416

Qy 414 ADELKADNKKSSFTPPVLSGGKLLQKGVTLBSTSQAEGSLGMDSTTLLTAGS 4737

Db 417 ANDPR---DFKSTIPQNVLSAGVYLKIKGAIVTVSKFTQSPGSHLYDLDTKLIAKED 4737

Qy 474 ITTNGINDSLGLKQPVSLAKAGSNKVI--VSGKMLIDIEGNIYESHMFSDOLFSL 5322

Db 474 IATIGLAIDTSLSSSTAAVITKANTANKQISVTDSIELISPTGAAVEDLRNRSOTFPL 5333

Qy 533 LKITTVDADVDTNDYDISLLIPVAEDPNSEYFGQGMNWNMTTDTATNTKEATATWTKGF 5922

Db 534 LSLLEPAGGSVYTTADPLPV-----SPHYGQGWKLAW---TOTGNKVGEPFWDKINY 5655

Qy 593 VSPERKSAVLCNTLNGVFTDIRLSLOLVEIGATGMEHKQGFVWSSMTNPLAKTGDENRK 6522

Db 586 KPRPEKRGMLVPRIILGNADVRSIMQVDETHASSLQDRGLMTDIGNLPHVASASDNI 6454

Qy 653 GPHRTGGYVIG--GSAHTRKDDLFTFAFCHLFAKXOCFIANNSSRYTGGTLFPHSHNTL 7111

Db 646 RYRHNSGGYVLSVNNETPR--HYTSMAFQLFPSRKQDVAVSNNEXRYMLGSLYQYTTSL 7044

Qy 712 -----QPNVYTLGRAKFSESALIEKFPREIPLADVDVSPSHDNRETHYTLPE 7622

Db 705 GNIFRYASRNPNNVGLILSRRLQNP-----MTHFLCAVGHANMDKDTYANAFPM 7566

Qy 763 SEGSMNSCTIAGIGLIDLPFLVSNPHPLFKFTIPQMKVEMYVVSQNSFESSSDGRFSI 8222

Db 757 VKMSMRNKCALIECGSMPLLVFENGRLPQGAIPFMKLQLVYAYQGDPEKTTADGRFSN 8166

Qy 823 GRLLNLSIPGAKFVQGDIGDSYTTDLGSEFFSVDYRRNNPOSTATLVMSPSMKIRGNL 8622

Db 817 GSUTSISVPGIRFETKLALSDQVLDVFSYSYIPDIRFDPSCEALVLSGDSWLVPAHV 8766

Qy 883 SPQAFLLRGSNNVYVNSCELFGHAYAMELRGSSRRYVNDVCTKLRF 928

Db 877 SRDAFVSGSTRHFNDYTELLCRGSIIECRPHARYNINCSKRRF 922

RESULT 13

US-09-438-185A-451

: Sequence 451. Application US/09348185A

: Patent No. 6822071

: GENERAL INFORMATION:

: APPLICANT: Stephens, Richard

: APPLICANT: Mitchell, Wayne

: APPLICANT: Kaiman, Sue

: APPLICANT: Davis, Ronald

: APPLICANT: The Regents of the University of California

: TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

: FILE REFERENCE: 018941-000411US

: CURRENT APPLICATION NUMBER: US/09/438,185A

: CURRENT FILING DATE: 2002-03-13

: PRIOR APPLICATION NUMBER: US 60/108,279

: PRIOR FILING DATE: 1998-11-12

: PRIOR APPLICATION NUMBER: US 60/128,606

[illegible]

```
; SEQ ID NO 474
; LENGTH: 643
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-474
```

```
Query Match      26.9%; Score 1286; DB 2; Length 643;
Best Local Similarity 41.5%; Pred. No. 2.5e-88;
Matches 268; Conservative 117; Mismatches 229; Indels 32; Gaps 10;
```

```
QY 295 GGFPEFLRNVSATKPGKGAISIDASGELSLSAETGNITFVTRTLLTTSSTDPKRNAI 353
DB 18 GGGISFNNNTVQGTGAAGAISSILAAGECSLSAAGDITFNGAIVAT-TPQTTKXNSI 76
QY 354 NISNGKFTELRAKNHTIFFYDPTSR--GTSADVLIKINNGSAGALNPYQGTLLFSGET 411
DB 77 DIGTAKITNIRALSGHSIFPYDPTANTADSTDTLNLKADAGNSTDVSGLVPSGEK 136
QY 412 LTADELKVDNLKSSFTQVPSLSGGKLLQKGVLTLESTFSQEAAGSLIGMDSGTTLSSTA 471
DB 137 LSEDEAKVADNLSTLQKQVTLTAGNLVLRKGVTLDTKGFTQTAGSSVIMDAGTTLKAST 196
QY 472 GSITTTNLGINVDSLGKQPVSLTRAKASNKVIVYSKLNLDIGNTIYESHMFSDQLFS 531
DB 197 EEVTLTGISIPVDSISGEGKKVIAASAAXKVALSGPILLDNGAMYENHDLCKTQDFS 256
QY 532 LKKTIVADVDYTNDISLIPVPAEDPNSSEYFGOGNNVMTTDTAT--NTKEATATWTX 589
DB 257 FVQJSA-LGTATTTDVRP---VPVATPTTHGYGCTGCMTAVDDTASTPKTKATLAWTN 312
QY 590 TGVPSPERKSAVNTLMGVFTDIRSLQQLVEIGATGMEHKGFVWSMTNPLHKTGDE 649
DB 313 TGYLPNPERQGPLVNSLIMGSFSDIQALQGVIERSSALTLICSDRGFMAGVANFLDKDKG 372
QY 650 NRKQPRHTSGGVVIGSGAHTPKDLPFAFCHLFAKDQCIIANNSTRTYGLTFEFGSH 709
DB 373 EKRRYRHSGGVYALGGAQTCSENLISPAFCQSGSDPLVAKNHDYTAGAAYIHHIT 432
QY 710 TLQONVYLRGRKPFSESAIEKFP---REIPLADVOVSFSHSDNRMETHTYSLPSEBS 766
DB 433 EC-----SGFIGCLDLKLPQSMHKLVEGQLAYSHVNDLTKTKTAYPEYKGS 482
QY 767 WSNECIAGIGLDLPVLSNPHP---LKFTHIPQMKVEMYVVSQNSFEBSSDGRGFSI 822
DB 483 WGNNAFMMMLGAS-----SHSYPEYLHCFDYAPYIKNLTYIKQDSFEKGTGRSFD 537
QY 823 GRNLNLSIPVAKPQVQIGDSYTYDLSGFFVSVDYRRNPOSTATLVMSPPSMKIRGNL 882
DB 538 SNLFNLSIPVGVKKEKFSDCNDFSYDLTLSTYVPLIRNDPCTTALVLSGASWETVANNL 597
QY 883 SRQAFLEGSNNVYVNSNCELFHGYAMELRGSSRRYVNDVGTCLRF 928
DB 598 ARQALQVAGSHYAFSPMFVULGQVFPEVRGSSRLTYNDLGGKQCF 643
```

RESULT 15
US-09-438-185A-455
Sequence 455, Application US/09438185A

Patent No. 6822071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kaiman, Sue
APPLICANT: Davis, Ronald
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08

```
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 999
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0453
US-09-438-185A-455
```

```
Query Match      26.9%; Score 1284.5; DB 2; Length 999;
Best Local Similarity 32.8%; Pred. No. 6.1e-88;
Matches 332; Conservative 163; Mismatches 393; Indels 125; Gaps 27;
```

```
QY 1 MKTSIWMVLVSVLAFSCHLOSILANEELSPDSEFNGNIDSGTFPTKS----ATTYSL 55
DB 27 MKTSIRKFLISTLA-PCFASTAFVEVIMPSNPFGS--SGKIFPYTLSDPRGLCIF 83
QY 56 TGDVFFPEPKG-TPVLSDCFKQTTNLTFLNGHSLTFGFLDAGTHA-GAAASTTANON 113
DB 84 SGLDYLANLDNAISRSSSCFSNRAGALQILKKG--VPSFLNIRSSADGAALISSVTQN 141
QY 114 -----LTFSGFSLSDSSSTVT----- 134
DB 142 PELCPUSFSGFSOMIFDNCEBLSLTSASNVIPHASAIYATPMLFTNNDSILFYNNRGA 201
QY 135 GCGTLLSAGVNLNENIRK-LVVAQNFSTADGAIKG-ASFLLTGTSGDALFSNNSSTYK 192
DB 202 GFQAAIRGHSITILENTKSLFENGSGISNGALTSAAINLINNSAPVIFSTNAGIYG 261
QY 193 GAIAITTAGARI-ANNNGYRFLSNINASTSGAIDDEGTSILSNKKLYPEGNAKTT--- 248
DB 262 GAIVLTGSMVLTGNSLVGFVNN--SSRSGAIVANGNVTFSNNSDLTFQNNTPSPQNSL 320
QY 249 -----GGAI-CNTKASGP---ELIISNNKTLFASVVAETSGSAIH 286
DB 321 PAPPTPEPPAVTPLLGYGALCTPPATPPPGVSLTIGENSVTFLENIASBOGALLY 380
QY 287 AKKLALSSGFTFELNNVSSATPKGASIDASGELSLSAETGNITFVTRTLLTTSSTD 346
DB 381 GKISIDSNNSTIFLNTAG---KGAIAIPESGELSLSANGDILLFNKNLSITSG--- 433
QY 347 TPKRNAINISNGKFTELRAKNHTIFFYDPTSE---GTSADVLIKINNGSAGALNPYQ 403
DB 434 TPTRNSIHPFKDKNFATLGATQGYTLFYDPIRSDLSAASAATVAVPKASADAYGG 493
QY 404 TLIPSGFTLLPADLKYADNKKSFQPVPSLSGGKLLQKGVLTLESTFSQEAAGSLIGMDS 463
DB 494 TLIPSGFTLLPATBAIPANAFTLNQKLEGGTLLRNGATILNHNFTODEKSVIYMDA 553
QY 464 GTTLST-----TAGSITITNLGINVDSLGKQVSLTRAKASNKVIVSGKMLDIEGN 517
DB 554 GTTLATNGANNNDGATTLKLVINLDSLDGTAAAVVNVSTGALLTISGLIGLVKNSQD 613
QY 518 IYESH-MFSDH-QVLSLKTIVDADVDYTNDISLIPVPAEDPNSSEYFGOGNNVMTT 575
DB 614 CODHGWENKDLQVPLBELKATSNVTYTTDFSLGTVNGYQSD---YGYGTV--EFTID 668
QY 576 TATNTKATATMTKGTGVPSPERKSAIVCNTLMGVFTDIRSLQQLVEIGATGMEHKGF 635
DB 669 TTHTT--VTGNWKKGTGLPHERLAPLIPNSLWANNYDLAAVQASADQEDVPGKO-LS 725
QY 636 VSSWTFELAKTGDENRKGRPHRTSGGVYIGSAHTPKDLPFAFCHLFAKDQCIIAANN 695
DB 726 ITGTTNFHANHGDASRYHMGGVLYINITYTITPDAALSLFGQLFTGSKYLVQGH 785
QY 696 SRTYGGTLFFKHSHTLOPQNYLRLGRKPFSESAIEKFPREIPLALDVQVSFSHSDNRET 755
DB 786 SNVFAIVYGNITKSL-----FGSSRFSGGTSR-----VTYSSNSNEKYKT 826
QY 756 HTYSLPESGSMWNECIAGIGLDLPVLSNPHPLFTFPIQMKVEMYVVSQNSFFESS 815
DB 827 SYTKLPGRCSWNNCWLGLBEGNLPITLSSRIINLKQIIPVKAQVAVYTHGIGQENTP 886
```


This Page Blank (uspto)

[illegible]

Query Match 3.9%; Score 187.5; DB 7; Length 1992;
Best Local Similarity 19.5%; Pred. No. 5.1e-05;
Matches 180; Conservative 125; Mismatches 350; Indels 269; Gaps 39

QY 4 SCFETPK---TSATFSLYTG-D-VFVYRPGKGTPLSDSCFQOTDNLTFELNGHSLFPGFI 96

Db 373 NATTTVKVSSSSSTTAELSDSLFTFOPNTGS-----QSRKTYVGVNGVKFT---N 421

QY 97 DACTHAGAAASTTANKNLTFSGFSLFSDSP-----STVTYGGOTLSAGVN 146

Db 422 NAEFTTAIGTRIRIRDKIGFARDODVDEKQAPYLDKKQLKVGSAVATIDNGI--DAGNKR 479

QY 147 LENIRKLIVVGNF-----STADGAIKAGSFLLTGTSODALFSNNSSSTKGAL 196

Db 480 ISNIAKSSADAVTIEQLKAKEFTLNAGA--GISVPTETISVDAKSGNATAPFYNIGVK 537

QY 197 TTAGARIANNYGVRFPSNIASTSGAIDDEGTEIISNNKFVPEGNAATTGGALCNTR 256

Db 538 TT-----ELNDDGTS---DKF-----SVK 553

QY 257 ASGSEPELLISNNKTLIPASNYA-----ETSGAIHAKKIALS 293

Db 554 GSGT-----NNSLTVAEHLASLYLNEVRNTADALQSFTVKEEDDDANAIVAKPTTK 606

QY 294 SGGTTEFL---KNVSSATPFGKAISIDAGELSLSAEFGNITFVANTLTGTSIDTPRK 349

Db 607 NAGAVSIILKLGKRGKGLTVATKQDVTV-----FGLSQDSG-LTIGASTNDDGLTVKDT 659

QY 350 RNAINISNG--KPELPLAAKKNHTFFYDPDTSEGTSDVLCINNKGSGALNPQGTLLFS 408

Db 660 NEOJQVGNAGNKKFTNNVGS-----NPTGIANTRAIRTRDKIGPFGS---DGAVDTN 707

QY 409 GETTLADELKVADNLKSSFTQPVSLSGGKLLQKGVTLLESTFSQZAGSLGMDSGTLLS 468

Db 708 KPYLDODKLG-VNK--ITNTGINAGGKAITGASPTLPSIADSSHNIEIGNTIDQDK 764

QY 469 TTAGSIT--ITNLGINVDSLGKQEVSLTAKGASKVYVSGKMLIDIEGNIYESHMSHD 527

Db 765 SNAASINDIILMTGPNL-----KNNNPIDFVSTYDVIDPANGNATTATVTHD 811

QY 528 QLFSLLKTTVDADVDTNVDISLLIPVPAEDPNSYFGQGNVNVMTDTFATNTKEATATV 587

Db 812 TANKTSKVYVAVND-----DTTHLHGTDDNKKLGVK-----TTKLNTKSANGN- 856

QY 588 TKTGVPSPERKSAJLVGNTLWGVFTDIRLSLOLVEIGATGMEHKQGFVWSMTNPLHKTG 647

Db 857 TATNNNNVSSDEDLV-----NAKDIAENLNTLAKEIHTTKGADADALQFTYKVV 907

QY 648 DENRKGFRHTSGGYIVIGSSAHTPKODDLFTFAFCHLPARDKDCFLAHNNSRYGGTLEFKH 707

Db 908 DENNNVA-----DDANAIR-----VGOKANNQVNTLLK 937

QY 708 SHTL-----QPNVYRLRPAKSESABE-KFP---REIPLALDVVSFSHS 749

Db 938 EGNGLNIKDKNGVTFYTGINTTSGLKAAGKSTLNDGLSKNPTSEQJQVAGAD-GVKRAKV 996

QY 750 DN-----RMEHTYT---SLPSESGWSNECI-AGGIGLDPFLVLSNPH 789

Db 997 NNNGVGAGIDGTTIRITRDEIGFTGNGSLDKSRPHLSKODINAGKKI-----1045

QY 790 LFKTFIPOMKVENYVYVONSFFESSSDGRGSGICRLNLSIPVAGKVVQDIDGISTYYDL 849

Db 1046-----TNIOGSHIAONS-HDAVTGKGIVDLKTELENNKISSTAKTAONSIFEFVADE 1096

QY 850 SG--FFVSDVYRNNPQSTATLWMS 871

Db 1097 QGNNTVSNPFYSYDTSKTSQVIT 1120

RESULT 3
US-11-013-759-4
Sequence 4, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping

```

; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-4

```

```

Query Match      3.9%; Score 187.5; DB 7; Length 2047;
Best Local Similarity 19.5%; Pred. No. 5.3e-05;
Matches 180; Conservative 125; Mismatches 350; Indels 269; Gaps 39;

```

```

41 SGTFTPK---TSATTYSLTGD-VFYPEPGKPTPLSDSCFKQTDDNLTFLGNGSLTFPGFI 96
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
428 NATTTVAVGSSSTTALBLSLFTQPNIGS-----QSTSKTYVGNGVKFT---N 476
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
97 DAGTHAGAAASTANKNLTFSGFSLSPDSSP-----STVTYTGQTLSSAGVN 146
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 NAETTAIGTRITRDKIGFARDGDVDEKQAPYDKKQKLVKGSVALITDNGI--DAGNKK 534
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
147 LENIRKLVAAGNF-----STADGAIKGASFLLTGSGDALFNNSSSTKGGAIA 196
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
535 ISMLAKSSANDAVTIEQLKAAPKPLNAGA--GISVTPTEISVDAKSGNVTAPYNGIVK 592
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
197 TTGARIANNNGYVRFPLSNIASTSGAIDDEGTSILSNKFLYFEGNAAKTGGALCNTK 256
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
593 TT-----ELNSDGTG---DKF-----SVK 608
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
257 ASGSPELIISNNKTLIFASVNA-----ETSGAIIHAKKLALS 293
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
609 GSGT-----NNSLVTAHLASYLENVRTADSAIQSTVKEEDDDANAIVAKDTTK 661
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
294 SGGTFTFL---RNNVSATPKGALISIDAGSLSAETGNITFVRNLTITGSGTTPK 349
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
662 NAGAVSILKLGKNGKLVATKKDGTV-----FGLSQDSG-LTIGKSLTNDGLTVKDT 714
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
350 RNAINIGSNG-KFTELRAAKNHTIFFYDPTISBEGTSVDVKINNGSAGLNPYQGTILFS 408
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
715 NEQIQVANGIKFTVNGS-----NPGTGIANTARITRDKIGFAGS---DGAVDIN 762
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
409 GETLTADDELKVDNLKSSFTQPVSLSGKLLQKGVLTLESTSPSQEAGSLGMDSGTTLIS 468
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
763 KPYLDQKLVQV-NVK--ITNTGINAGKALITGLSPTLPISADQSSRNIELGNTIQDKK 819
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
469 TTAGSIT-ITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSD 527
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
820 SNAASINDIINTGHNL-----KNNNPIDIPVSTYDIVDPANGNATTAATVATHD 866
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
528 QLESILKITDADVDNVDISSLIPVAPDPSSEYGGQGMVNWMTDTATNTKEAATVW 587
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
867 TANKTSKVYDVAVND-----DTTHTLTGTDNKKLGAVK-----TTKANTKSAGN- 911
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
588 TKTGFPVSPERKALVGNLTMGVFTDTRSLQQLVELIGATGMEHKQGFVWSMTNPLHKTG 647
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
912 TANTFNVNSSDDBALV-----NAKDLAENLNNTLAKIHTTKGTADNALQTFYKVV 962
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
648 DENRKGFRHTSGGVVIGSAHTPKDGLFTFAFCHLPARDXOCPIAHNNSSTYGGTLFFK 707
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
963 DENNNA-----DDANAAT-----VGKANNQVNTTLK 992
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
708 SHTL-----QPNYLRIGRAKFSASAIF-KFP---RELPLALDVQVVSFHS 749
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
993 ENGLNITKDKNGVTTFGINNTSGLKAKSKTLNDGSLIKMPTGSEQIQVAVD-GVFKAKV 1051
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
750 DN-----RMEHTYT-----SLPESEGSWSNECI-AGGIGLGLPFLVSNPH 789

```

```

DB      1052 NNNGVAGIDGTRITRDEIGFTGNGSLDGSKPHLSXQGINAGGKKI----- 1100
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      790 LFTFTIPQKMEVENVYSSNFFESSDGRGFSIGRLNLTSPVGAFFVGIDSDTYDL 849
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1101 -----TNIQSGEIAQNS-HDAVTGKTYDLKTELKNTSISTAKTAQNSLHEFSVADE 1151
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      850 SG--FPVSDVYRNNPOSTATLYWS 871
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1152 QGNFTVSNPYSSYDTSKTSDVIT 1175
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 4
US-11-013-759-7
; Sequence 7, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loomis, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-7

```

```

Query Match      3.9%; Score 187.5; DB 7; Length 2047;
Best Local Similarity 19.5%; Pred. No. 5.3e-05;
Matches 180; Conservative 125; Mismatches 350; Indels 269; Gaps 39;

```

```

41 SGTFTPK---TSATTYSLTGD-VFYPEPGKPTPLSDSCFKQTDDNLTFLGNGSLTFPGFI 96
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
428 NATTTVAVGSSSTTALBLSLFTQPNIGS-----QSTSKTYVGNGVKFT---N 476
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
97 DAGTHAGAAASTANKNLTFSGFSLSPDSSP-----STVTYTGQTLSSAGVN 146
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 NAETTAIGTRITRDKIGFARDGDVDEKQAPYDKKQKLVKGSVALITDNGI--DAGNKK 534
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
147 LENIRKLVAAGNF-----STADGAIKGASFLLTGSGDALFNNSSSTKGGAIA 196
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
535 ISMLAKSSANDAVTIEQLKAAPKPLNAGA--GISVTPTEISVDAKSGNVTAPYNGIVK 592
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
469 TTAGSIT-ITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSD 527
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
593 TT-----ELNSDGTG---DKF-----SVK 608
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
257 ASGSPELIISNNKTLIFASVNA-----ETSGAIIHAKKLALS 293
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
609 GSGT-----NNSLVTAHLASYLENVRTADSAIQSTVKEEDDDANAIVAKDTTK 661
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
294 SGGTFTFL---RNNVSATPKGALISIDAGSLSAETGNITFVRNLTITGSGTTPK 349
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
662 NAGAVSILKLGKNGKLVATKKDGTV-----FGLSQDSG-LTIGKSLTNDGLTVKDT 714
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
350 RNAINIGSNG-KFTELRAAKNHTIFFYDPTISBEGTSVDVKINNGSAGLNPYQGTILFS 408
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
715 NEQIQVANGIKFTVNGS-----NPGTGIANTARITRDKIGFAGS---DGAVDIN 762
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
409 GETLTADDELKVDNLKSSFTQPVSLSGKLLQKGVLTLESTSPSQEAGSLGMDSGTTLIS 468
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
763 KPYLDQKLVQV-NVK--ITNTGINAGKALITGLSPTLPISADQSSRNIELGNTIQDKK 819
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
469 TTAGSIT-ITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSD 527

```


Db	820	SNASINDILNTGFWL-----KNNNFIDFVSTYDVIYDPFANGATTATYTHD	866
Qy	528	QLFSLKTIYDADVDYNDVLSLIPVPAEDNSEYFQOGNNVWTTDTATNTREATATW	587
Db	867	TANTSKVYVND-----DTTILHTGTDNKKLGXV-----TTLKNTSANGN-	911
Qy	588	TKTGVPSPERKALVCNTLNGVFTDIRLSLOOLVEIGATGEHKGQFVWSMTNPLKGTG	647
Db	912	TATPNVWSDEBALV-----NAKDIEMENITLTAKEIHTTGTADTLAQTFYVKKV	962
Qy	648	DENKGFHTSGGYVIGSSAHTPKDULTFPAFCHLPADKOCFLAHNSRYYGGLPFKX	707
Db	963	DENNNA-----DANAIT-----GQKANNQVNTLLKQ	992
Qy	708	SHTL-----QPNVLRLEGRKESSEAIK-KFP---REIPLADVOVSFSHS	749
Db	993	ENGLNIKTDXKGYTFYFGINTTSGLKAKGASTLNDGSLKNTPTGSGQIDVGAD-GYKPAKV	1051
Qy	750	DN-----RMEHTYT-----SLPSESGWSNECI-AGGIGLDLPVYLSNPH	789
Db	1052	NNNGVAGCIDOTTRITRDEIGFTGTSNLSDKRHLKSXDGJNNGKKI-----	1100
Qy	790	LFKTFIPOMKVBMYVVSQNSPFRESSDORGSIGRLNLSLPVGAKFYQSDIGDSYTYDL	849
Db	1101	-----TNIGSGEIAONS-HDAVTGKGKIDYDLKTELENKISSTAKTAQNSLHEFSVADE	1151
Qy	850	SG--FFVSDVYRNNPOSTATILVMS	871
Db	1152	QGNNTVSNPYSSYDTSKTSIDVT	1175

```

RESULT 5
US-11-013-759-9
; Sequence 9, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Saaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-9

Query Match          3.6%; Score 172; DB 7; Length 2053;
Beet Local Similarity 21.7%; Pred No. 0.00056;
Matches 182; Conservative 108; Mismatches 307; Indels 242; Gaps 42

QY      42  GNTPKTSATVTLTGDFVFEPKG--TPLSDSCFKQTDDMLRFLNGHSLTFGFI DAG   99
        ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      1209 GTTTKRLTVGNNGNGGIIVINSQGNTITGLSNTLANVTNDR-----GSVRTTQCNIIKD 126

QY      100 THAGAAAS---TTANKULTBEG-----FSLISFDSSPSTVYTGGGITLSAG---- 143
        ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      1265 EDKTRAAASIVDVL$AGFNLOQNGEAVDFVSTVDYNFAFGNTITAKVIYDDITSKTSKVY 132

QY      144 GVNLENI-----RLVVANGSPSTADG-GAIKGASFLILGTSGDLLFSNN-----SFTKG 192
        ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      1325 DVNVDDTTIEVDKDKLGAVTTTTLTISTGTANKPA--LNSQATGDALVKRASDIVAHNIUTLS 138

QY      193 GAATTAGARIANNTGYVRFLSNIASTSGAIDDEGTSIL---SNNKFLPYEGNAKTGG 249

```

```

Db      1383 GDICTAGASGANN-----SAGVADADGNKVIYDSTDNK--YYQAK-----ND 1423
Qy      250 GAICNTYASGSPELIIS-----NNKTLIPASNVAETSGCAIHAKKALIS-SGGF 297
Db      1424 GTVAKTEKVAADKLVAAOQTPEDTGLAOMNYSVINKQVANDAN-----KKOGINEDNAF 1477
Qy      298 TEFLLRNWVSATPKGAISITDASELSLASETGITFEVRNTLTFTT-----GSTD 346
Db      1478 VKGLEKASDNKTKMAAVT---GDIAVAOQT-PLTFAGDTGTTAKKLGETLITIKGGQTD 1533
Qy      347 TPKENAINIG--SNGKFEELRAAKNHTIFPYDITSEGTSSDVLKTN---NCSAGALN 399
Db      1534 TNKLTUNNIGVAAQTDEFT-VKLAKDITNL--NSVNAAGTKRIDEKGISFVADANQOAKANT 1590
Qy      400 PYQGTILFSGEITLFADELKVAADNKSSEFTQVSLSGAKLLQKQVTLTESTSFS-----QE 454
Db      1591 P-----VLSANGIDL-----GGKVISNVGKGTKOTDIAAVOQUNE 1625
Qy      455 AGSLIGMDSCTLTSTTAGSITI---TNLGINVDSLGLKOPVSLTAKASN--KVIYSQKL 509
Db      1626 VRNLILGINDADNQNVIADIKDPPNSGSSSNRTVIKAGTVLGGKNNPTDEKLATGAVQ 1685
Qy      510 NLIDIEGNIYE--SHMF--SHDQLFLKLTVDADVDTWVDSLSLVPVPAE-----556
Db      1666 VGVDKDXGANGDLSNVWKTOKQDOKSKALLATTYAAAOQTIYVYN---PAEALDRINEQ 1741
Qy      557 -----DPNSEYGFQGOQNNVNNTTDTATNTKEATLTWTKTGFPSPERKSALVNTLW 608
Db      1742 GIRFEHVVDNGQEPVVGQNGRI---DSSASGKHSVA---IGFOAKADGEAAV-----1787
Qy      609 GVTFPDIISLQOLVETLQATGCMHKQGFVWVSMTNLLHKTGDE-----NKRGPHTSGGY 661
Db      1788 -----ALGRQTOHQNGOSIALGDAAOATGDDOSIALIGTGNVYVAGHSG--1828
Qy      662 VIGGSAHTPKDLETFAPCHLF--ARDKCEIAHNSRTYGGTLFPKSHTLQPONYLRL 719
Db      1829 AIGDPSTVKADNSYSVGNNGNQFTDATQCDVAGVGNNI-----TVTESNVAL 1875
Qy      720 GRAFSESAIKFREFRILADVDVSPSHSNRMETHY-TSLPSEGSWSMECIAIGIG 777
Db      1876 G-----SNSAIS-----AGTHAGTOAKKSDGAGITTTAGATG 1908

```

```

RESULT 6
US-10-485-517-252
; Sequence 252, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-252

```

Query Match 3.6%; Score 171; DB 1; Length 761;
Best Local Similarity 20.0%; Pred. No. 0.00017;
Matches 106; Conservative 114; Mismatches 232; Indels 78; Gaps 18,

QY 21 QSLANEELSPDPFNGNIDSGTTPKTS-----ATTYSLTG-----DVFPEPKGTPL 70
DB 267 QSTQSSESTSTSTLS---DSTSISKSTSGSVSTASLSGSESESDSGSSTASSEST 323
QY 71 SDSGCKTNTNLTLFGHSLTFPGFIDAGTAGAASTANKLTFG--GFSLSFDS 129
DB 324 SESASTLSLSDSTSTSGSAST--STLSNSASASEDLSTLSLSDSTASMSQSESDSQ 381
QY 130 TTVVTCGGLTSAGVNLLENIRKLVAAGNFSTADGAI-----KGAFL 173
DB 382 STASLSLSDSTSTSNMSTASL--STSVSTSESGSTSESTSDSTSTLSMSQSTSR 439
QY 174 LTGSGDALFSSNNSSTKGAIAITTAARLANNTGYVFLSNASTSGAIDEGTSL 233
DB 440 STSASGASTSTSTSDRSTASSTSMRTSTSDQMSLSTSTSTG---MSDSTSLSD 495
QY 234 NNKFLYEGNAAKTGAICNTKASGSPBELISNNKFLIPASNAVEISGAIAHAKKALS 293
DB 496 SVSDSTSDSTGAST-----SGSMVSAISLSDSTSTSTASSEVMSASISDSQMSSE 545
QY 294 SCGFTEFL--RNNVSATPKGAISIDAGELSL-----AETGNITFVANTLT 342
DB 546 SVNDSSEVSSENSGSDSKMSGTSVSDSGSLSTLRKSESVSESSSLSCSQMSDSV 605
QY 343 GSTDTPKRNAINIGSNKFTELRAAKNHTTFYDPT--SEGTSSDVLKINNGSAGALNPY 401
DB 606 STDS---SSLVS-----TSLRSE--SVSESDLSLSDSKSTSGSTSTSTSTSL 655
QY 402 QGTLFGEFLTADLKVADNLS---SFTQPVLSGGKLLQGVTLSTSTSTSTST 457
DB 656 SGSESVSESTLSDSISMSDSTSTSDSLSGSISLGSSTSLSTSDSLSTSTSTSTST 714
QY 458 LLDGMSGTTTSTAGSTITINLGINVDSLGLKOPVSLTAKGASNKVIVSG 507
DB 715 MSGSESTSTSVSDSGSSTSTNSQFDSMSISASESDMSSTSDSS---ISG 761

RESULT 7

US-11-013-759-11
; Sequence 11, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS.Jb
; CURRENT APPLICATION NUMBER: US/11/013, 759
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361, 619
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2314
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-11

Query Match 3.5%; Score 169.5; DB 7; Length 2314;

Best Local Similarity 20.5%; Pred. No. 0.00096;

Matches 178; Conservative 99; Mismatches 289; Indels 303; Gaps 40;

QY 42 GTTPKTSATTVSYLTGDFVEPEPKGTPLSDSCFKQTTDLNLTFLGNSHLTFGFIAGTH 101
DB 1143 GLTTPKLTVAANNKGKIVIDSKQNTITG---LSNLTAVNTDGAHALSGGLAN-DTD 1198
QY 102 AGAAS---TTANKNLTFSG-----PSLSF--DSSSTVTTTGGGLSSAG----- 143
DB 1199 KTRBASIGDVLANGFNLQNGEAVDFVSTYDTVDIFDGNATTAKVITDPTSKTSKVYDV 1258

QY 144 -----GVNLLENIRKLVAAGN---FSTADGAIKGAFLTLTGSGDALFSN 185
DB 1259 NVDNKTLEVTSDKDLGVKTTTLTKTSANGATKFSADGDALVKAADIAT----- 1308
QY 186 NSSSTKGAIAATTAARLANNTGYVFLSNASTSGAIDEGTSL--SNKFLYEGN 243
DB 1309 -HUNTLAGDIQTAKA-----SQASSASAYVADANKYIYDSTDK-KYYQVN 1353
QY 244 AAKTGAICNTKASGSPBELIS-----NNKTLIPASNAVEISGAIAHAKKALS 292
DB 1354 ----DKQVYNKKEVAKDKLVAQAQTPDGTLAGMNVKSVINKEQVANDAN-----KQGI 1403
QY 293 S-SGCFTEFLRNNVSATPKGAISIDAGELSLAETGNITFVANTLT 342
DB 1404 NEDNAFIKLENAKDKTKTGNAAVTV---GDLNAAVQT--PLTFAGDTGTAKKLGFTLTI 1459
QY 343 --GSTDTPKRNAINIG--SNKFTELRAAKNHT-----IFPYD----- 377
DB 1460 KGGQDTNKLTDNNIGVACTDFT--VKLAKDLTNLSVNAAGTRIDEGKISFVDANGQA 1518
QY 378 -----ITSEGTSSD-----VLKINNGS-AGALNPY- 401
DB 1519 KANTPVLSANGLDLGKRLSNIGAAVDDNDVAVFKQPEVAKTVNNLNQNSGASLFPV 1578
QY 402 -----QGT-----ITSEGTSSD-----ITSEGTSL 412
DB 1579 VTDANGKPINGTDGKQKAIKGADEKYYHANANGVPEVDKGPITDADKLANTLAHGKPL 1638
QY 413 TADELKVAD-----NLKSTQPVLSGGKLLQGVTLSTSTSTSTSTSTST 461
DB 1639 DAGHQVVASLGNSDAITLTINIKSTLPQIDPTPTGNANNGAQSLSTSLSAQO----- 1691
QY 462 DSGTTLSTTAGSTITINLGIN-----VDSLGLKQPVSLTAKGASNK 502
DB 1692 ----SMAASVQDVLANGFNLQTNNOVDVFKAYITVANFVNGTGADITSVRSADGTMSN 1745
QY 503 VIVSGKLNLDIEGNTY---ESHMFSDOLF--SL--KITVDADVNTVDISLIPV 553
DB 1746 ITVNTALAAATDDGAVNLIRAKDGKFKKADLWNGSLKKGKASDAKTPGL--SLV-- 1800
QY 554 PAEDNSEYGFQOQ-WNVNMTTDTAINTKATATWTMTKTGVPSPERK----- 599
DB 1801 ---NPNAGKSTDAVALNNLSKAVFKSKDGTITTVSSDGLSISQKDNSSITLSKQGLN 1857
QY 600 --SALVONTLMGV-FPDIRSLQOLVEI-----GATGMEHKQGFWSMTNPLHKTGDN 650
DB 1858 VGGKVISNKGKGTXTDAAVQQLNEVRNLGLIGNAGNDNADG---NOVINADIKKDPN 1913
QY 651 RKGFRTS---GGYVIGSAAHTPKDDLFT 676
DB 1914 SGSSSRVTYIKAGTVLGKGNNDTEKLAT 1942

RESULT 8

US-10-485-517-324
; Sequence 324, Application US/10485517
; Publication No. US2005025629A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexis Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629MO
; CURRENT APPLICATION NUMBER: US/10/485, 517
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 324

LENGTH: 496
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-485-517-324

Query Match 3.0%; Score 141.5; DB 1; Length 496;
Best Local Similarity 18.8%; Pred. No. 0.0086;
Matches 93; Conservative 70; Mismatches 21; Indels 121; Gaps 13;

QY 169 GASFLTGT-SGDALFSSNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGAIDDE 227
DB 17 GVASVLVGLIGFGLSSKEADASENSVTQSDASNESSSSVSAAPKTDITVSDT 76
QY 228 GTSLISNNKFLYFEGNAA--KTTCGAICTKASGSEPELLISNNKTLIFASNVAETSGAI 285
DB 77 KTSNTNNGETSVAQNAQOETTOSSTNATTEETPTGAEATTTTNQANTPATTOSSNT 136
QY 286 HAKKALSSGGEFFL-RNNVSATPKGASISIDASELSAETGNITFVRNTLTGGS 344
DB 137 NAEELVNOTSNETTENDTNTVSVSPONSTNAE--NVSTTODTTEATPSSNESAPOS 193
QY 345 TDTPKRNAINIGSNGKTEFLRAKNHTIFFYDPTISGTSDDVLKINNSAGALNPYQGT 404
DB 194 TDASNKDVNOAVNTSAPRMA-----NVT-----VGIDSG 246
QY 405 ILFSGETLTADDELKVADNLKSSFTQPVLSGGKLLQKGYTLBESTSFQEGSLLGMDSG 464
DB 216 --FSLAAVADAPAAAGTDITNQLT-----NVT-----VGIDSG 246
QY 465 TTSTAGSITITNLGINVDSLKQPVSLTAKASNKVYSGKLNLDIEGNIYESHMF 524
DB 247 TTVYPHAGYVKLVNPGSPNSAV-----KGDTEFKITVPKELNNGVSTAKVPPIM 298
QY 525 SHDQFLSLKITVDAD-----VDTNVDISLLPVPAAE-DPNSSEYGGQGMNVMWT 573
DB 299 AGDQV--LANGVIDSDGNVYTFPTDYVNTKQDVAKALTMPEYIDPE----- 342
QY 574 TDATNTKEATATWTKTGFVSPERKSALVNTLMGVFTDIRLQOLVEIGATGMEHQG 633
DB 343 ----NVKKTGNVTLATIGISTTANKTYLVDEYKGFYNLISIGTIDQIDKTNNTYRQ- 396
QY 634 FWSSMTNPLHKTGD 648
DB 397 -----TIVVNPBGD 405

RESULT 9
US-10-485-517-325

Sequence 325, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynex Incorporated
APPLICANT: Foster, Simon
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PatentIn version 3.1
SEQ ID NO 325
LENGTH: 496
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-485-517-325

Query Match 3.0%; Score 141.5; DB 1; Length 496;
Best Local Similarity 18.8%; Pred. No. 0.0086;

Matches 93; Conservative 70; Mismatches 21; Indels 121; Gaps 13;

QY 169 GASFLTGT-SGDALFSSNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGAIDDE 227
DB 17 GVASVLVGLIGFGLSSKEADASENSVTQSDASNESSSSVSAAPKTDITVSDT 76
QY 228 GTSLISNNKFLYFEGNAA--KTTCGAICTKASGSEPELLISNNKTLIFASNVAETSGAI 285
DB 77 KTSNTNNGETSVAQNAQOETTOSSTNATTEETPTGAEATTTTNQANTPATTOSSNT 136
QY 286 HAKKALSSGGEFFL-RNNVSATPKGASISIDASELSAETGNITFVRNTLTGGS 344
DB 137 NAEELVNOTSNETTENDTNTVSVSPONSTNAE--NVSTTODTTEATPSSNESAPOS 193
QY 345 TDTPKRNAINIGSNGKTEFLRAKNHTIFFYDPTISGTSDDVLKINNSAGALNPYQGT 404
DB 194 TDASNKDVNOAVNTSAPRMA-----NVT-----VGIDSG 246
QY 405 ILFSGETLTADDELKVADNLKSSFTQPVLSGGKLLQKGYTLBESTSFQEGSLLGMDSG 464
DB 216 --FSLAAVADAPAAAGTDITNQLT-----NVT-----VGIDSG 246
QY 465 TTSTAGSITITNLGINVDSLKQPVSLTAKASNKVYSGKLNLDIEGNIYESHMF 524
DB 247 TTVYPHAGYVKLVNPGSPNSAV-----KGDTEFKITVPKELNNGVSTAKVPPIM 298
QY 525 SHDQFLSLKITVDAD-----VDTNVDISLLPVPAAE-DPNSSEYGGQGMNVMWT 573
DB 299 AGDQV--LANGVIDSDGNVYTFPTDYVNTKQDVAKALTMPEYIDPE----- 342
QY 574 TDATNTKEATATWTKTGFVSPERKSALVNTLMGVFTDIRLQOLVEIGATGMEHQG 633
DB 343 ----NVKKTGNVTLATIGISTTANKTYLVDEYKGFYNLISIGTIDQIDKTNNTYRQ- 396
QY 634 FWSSMTNPLHKTGD 648
DB 397 -----TIVVNPBGD 405

RESULT 10
US-10-793-626-1780

Sequence 1780, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P13480US
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1780
LENGTH: 1155
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-1780

Query Match 2.9%; Score 140.5; DB 1; Length 1155;
Best Local Similarity 22.7%; Pred. No. 0.031;
Matches 141; Conservative 72; Mismatches 203; Indels 205; Gaps 35;

QY 33 DSENGNIDSGT-----FTPKTSATTYSLTGDFVFEYEPKGPPLSDSCRTQTDNLFL 85
DB 581 DSEFNDLSSNVXDVTQSFTPKVSA-----DGRPV-DINPARSVAN----- 620
QY 86 GNGHSILTFGFIDAG-----THAGAAASTANKXULTFSGFSLSDSSPSTVT-----T 134
DB 621 GKXIVVQAVAPRTGTGNVYTEYWLTRDGTNTDFYRG-----TKSTIVYVYVYVNGSST 672

```

OY      135 GOG---TSSAGCVLLENIRKLV-----VAGNSTADGGAIKASFLRTQTSDALFS 184
Db      673 AOGDNPTSLSDGYVWLKKNKXGVQDDDEKGLAGVYVTLKDSNNRLQGVTTDQSHGYFD 732
OY      185 NNSSTKCGAIAATTAGARIANNTGYVRLPUSLNIASITSGAIIIDEGSTIISNNKFLYFEGNA 244
Db      733 N-----LONGTYVFEF-----AIPDNYTPSPANN-----756
OY      245 AKTTGCAI-CNTKASGPELLIISNNKTLIPASNVAFSTGGAIIHAUKALSSGCFTEPLRN 303
Db      757 --STNDALIDSDEGERGTRKVVYAKG-TINMADMTVDITGFYITPK---YNGDY-----804
OY      304 NVSSATPKGGAISIDASGELSISAETGNIITFVRNLTITTSSTDTPKRNAINIGSKFTE 363
Db      805 -WVEDTNKDG---IODDNEKGIS--NVKYTLKKNKGDITGTTTT-----DSNGKY-E 849
OY      364 LRAAN--HTIEF-----YDPTISGTSDDVLKINNGSAGALNPQGTILFSGELLTDE 416
Db      850 FTGLENGDYITIEFETPEGYTP-TKONSGSDEKDSNG-----TKTIVT 891
OY      417 LKVADN-LKSSFTQPVSLSGSKL-----LQGVTLBESTSFQSEAGSLIAMD 463
Db      892 VYDADNKRITDGGFYKPIYVNLGDYVWEDTNKOGIODSEKGISGVKVTLLKDKNGAIG---948
OY      464 GTTLSTNA-----GSTI---TNLGINDSLKQPVSLTALGASNKRVVSGKL 509
Db      949 --TTTIDSGHYQFKGLENGSTYVEFETPSGTTPTKANSQGOITVDSNGITTTGIIINAD 1006
OY      510 NLIDIEGNIYESHMRFS-HDOFLSLKLITVDAVDVTINVAISLIPVADPNSSEYFQG--566
Db      1007 NL-TIDSGFYKTPKXSVGDYWE-----DTNKD--EKISGVK 1044
OY      567 -----QNNVNWTTDTATNTK 581
Db      1048 VTLKDEKGNIIISTTTDENGK 1068

```

```

RESULT 11
US-10-510-386-2
; Sequence 2, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
; US-10-510-386-2

```

```

Query Match 2.9%; Score 137.5; DB 1; Length 802;
Best Local Similarity 20.8%; Pred. No. 0.03;
Matches 141; Conservative 76; Mismatches 241; Indels 221; Gaps 34;

QY 62 YEP-----GKGTPL--SDSCFKQTTNDLPLTG-----NGHSLTFGEIDAG---THAGA 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 YKPSVVKKQDVTLAADALYPMQMDKSAPIFGADQAMKSGYTGKGIWVAIVIDIGVDYTH--- 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 105 AASTTANKLTLFSGFSLLSFDSSPESTVY-----TSGGT----- 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 193 --PDLKNNGFYKGYDPVNDYDPDEPTLPGRGATDGHGTHVAGTIAANGQIKGVAPEA 250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 139 -----LSSAGGVNLENIKRLVAG-NFSTRDGAATGASGLTLTGTSGD----- 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db      251 TLLAVRVLGPGSGTTEH-----VLAIGLEKAVADGAKWNLLSIGNSLNPDYATSIALDWA 306
QY      181 -----ALFSNNSSTKCGAIATTAAGAIANNTG-----YRFLSLNIASSTGCAI-----D 225
Db      307 MAEGVAVATSNNGNGPENMTWTSPTSRSVAISVGSOLPYREYVSVTLPSSYSAKMWGYOE 366
QY      226 DEGTSISNNKEFLYPE-----GNAKTTGGAIC-----NTFASGSPELI 264
Db      367 EKDLBALNGEVELVEAGLDGADDFSGCDVGVKXAVIORGVIIPFYDKAEMNAKNAIGAV 426
QY      265 ISNNKTLIPASNVAETSGCAIHAKKLALSSGGTFEPLNNVNSATPKGCAISIDASBELS 324
Db      427 IYNNATGEIEANV---KGMAMPYVLXKEEG---EKLVOQI-----KEGSHVSVPFKLD 475
QY      325 LSAETGNITF-----VNTLTFTTGSTDPKKNALINIGNKGFTELRAKNNHTIFFYDPI- 378
Db      476 KKLGETIASFSSRGPRVMDTMKIKDVASAP---GNVIVS-----TTPHDPKN 519
QY      379 -----TSEGTSDVLKINNGSAGAL-----NPFYO-GTILFSGETLT----- 413
Db      520 PYGVGSKQGTSMASPHV-AGTAAILLKQAKPWTBEQIIGVLMNTAKELTLDENGKRLPHNT 578
QY      414 --ADELKVADNLK--SFTQPVYSLSGKLLLOXG-----VTLESTPSQDEAGSLIGMDS 463
Db      579 QGASIRIMEALIKASSIVTTPGSHSYGTFLKQKQKQTKKQAKFTIEHLSHRKAYVOLEYSPK 638
QY      464 GTTUSTTAGSITITNNGINVDLSLQKOPVSLTAGASNKVIVSGKLNLIIDEGNLY---E 520
Db      639 GTGTI-TYSGTRRVV-----VPANOTGKAARAVYVNSAKTKAGTYEGVIYIRED 685
QY      521 SHMESDOLFSLK-----ITVDADVDTNV-DISSLIIPVPAED----- 557
Db      686 GRKVAEIPLLIIVKEPDYRVTSVTEPBGAKQAGYITAEVYLPGBAEELAFIVDENIMIL 745
QY      558 -----ENSEYGFQO-QWN 569
Db      746 GQAGVYRNQKGXGYOQWN 764

```

```

RESULT 12
US-11-091-643-18
; Sequence 18, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moritichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1332
; TYPE: PRT
; ORGANISM: Bacillus popilliae
US-11-091-643-18

```

Query Match	2.6%	Score	124.5	DB	7	Length	1332
Best Local Similarity	19.0%	Pred.	No. 0.43				
Matches	76	Conservative	64	Mismatches	165	Indels	95
						Gaps	14

```

Oy      201  ARIANNNGYVRFLSNIASTSGAIDDEGHSILSNKKFLYFEGNAKTTGAGICINTKASGS 260
      330  SRVYIDIGI-----LSTYIGGO-----YNNNFWRHTYQTLRTTGGTSFQSPITYGS 375
Db      261  PELIISNNKTLIPASNVAETSGGAIHAKKALSSGGFTEFLNNVSSATPEKGA1----- 315
      376  TAPPIQRTNLTFTSGDGVYTTIESVYTRSL-----YGNASVAFGTTGRSLYENPT 426
Oy      316  -----SIDASGELSIAETGNITV-----RNTLTGSGTDTPKKNAI 353
      427  VYEPFAOKLHIEHPGVD-SGRPNATVNSHLSYISGFSLGYSBPSGVLVGMTSTTATREN 485
Oy      354  NISNGKFEELRAAKNHTIFVDPDITSEB-TSDVULKINNSAGALNYQGTILFSGETL 412
      486  NITLDDRIVOLPRAVKASALNNCOVAKGTFTGGDWLAKPNNN--GTFSWY-----FAIRSA 538
Db      413  TADELKADWILKSSFTQPVLSGSGK-----LLLOKVTTLESTSFSGEAGSLGMDSGT 465
      539  YTHFRIRRVASSASFPSVISEBGRPTTVLFLSTMSPLQONDF--EAKTYVDLSTSV 566
Oy      466  TLSTTASGITTYNLGINVDSLKOPVSLTAKGASNKVIVSGKLNLDIEGNIVE----- 520
      597  TIRYTSASTTFQUNFR-----FTVSGSANVLI--DRIEFVPIEGLSEFEYETKO 643
Db      521  -----SHMFSHOULFSLLKITVDAVDVINDVSSLI 551
      644  QLEKARAVNVHLFTDSKALKEDTDTYDIEDAANVOCI 683

```

```

QY 326 SAEGNITFNRNLTITGSTDTPK---NNAINISNGKFTELRAAKHTIFVYDPIRSEG 3820
Dh 205 LAISGN-----KISGDVDSRCVMLEFLDVSNNRSTOI-----PFLGDC 2444
QY 383 TSSDVLKINNGSAGALNPOYGTILFSGTTLPADELKVDNIKSSFTOPV----- 4211
Dh 245 SALQHLDISG-----NKLSDG--FSRAISCTETKLLINISNOFVPIPLPLKLOYL 2366
QY 432 SLSGKULLLOKGVTLTESTF--SQEAGSLGMD--SGT-----TLSTAGSIT--ITNGLIYND 4844
Dh 297 SLIENF-----TGEIPDFISGACDTLTGLDSNHFYGAVPPFQSCSLLESIAISSN 350
QY 485 SLGKOPVSLTAKGANVKIYVSGKNTLIDIEGNIYESHMFSDQPLFSLKITVADVDTN 5444
Dh 351 NFGSELPMDLTKMRGLKVL---DLSNPFSELPES-----LTNLSASLLTLDISSN 4000
QY 545 VDISSLPYPAEDPNS-----EYFGQGMVNVMTDTIATNTRKATATWK---TGF 5922
Dh 401 NFGPILPNLCQNPXNTLQELYLONNGFTGK-----IPTLSNCESLVSLHSFNLYLSGT 4555
QY 593 VP-----SPERSALVCTLMGVTD---IRSLQOLV-----EIGATGNEHQGF 6344
Dh 456 IPSLSGLSLRDLKLTLMNMLEGEIPEOBIAMVYKLTLETLLIDPNDLTGEI--PSGLSNTNL 5144
QY 635 -WYSMTNPLAKRGD-----ENRKGFBRHSGGYVIGSANTPKDDLFTFACHLFEAR 6888
Dh 515 NWISLSNNRL--TGEIPKMGIRLENTALIKUSNNSF--SGNIPLAELDGRSLIYLDL--- 5666

```

```

RESULT 13
US-10-667-295-100
Sequence 100 Application US/10667295
Publication NO. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Maecia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11656-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIORITY APPLICATION NUMBER: US 60/411,823
PRIORITY FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 100
LENGTH: 1196
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURES:
NAME/KEY: VARIANT
LOCATION: (1)...(1196)
OTHER INFORMATION: Ceres Seq. ID no. 12653918
US-10-667-295-100

```

```

Db      568  -----NTNLFNGTIPAAAFKQSGKI-ANFIAGKRYVYIKNDGKKCKCHGAGNILE 617
QY      742  VQVSFSDSDRMETHHTLSLPESEGSWSNCE-----IAGIGLDLPVLSNHPLEFKTEIF 796
Db      618  FQGRISQQLRLSTR-----NPCNITSVYGG-----HTSPFFDNNGS 655
QY      797  QMKREMYVYSQNSPFESSDDGRGFSIGRLNLISIPVAKPVQGDIGDSYTYDLSGFVSD 856
Db      656  MFPLDMSYNNLSGYIKREIGSMPYLF-ILNL-----GHNDISGSIPE-VDGLRGLNILD 708
QY      857  VYRRNN-----POSTATLVNSPDQSKRGNLS 883
Db      709  LSSNKLDGRIPQMSALTWLTEL-DLSNNNLS 739

RESULT 14
US-11-074-176-12
: Sequence 12, Application US/11074176
: Publication No. US2005025015A1
: GENERAL INFORMATION:
: APPLICANT: Klaenhammer, Todd R.
: APPLICANT: Russell, William W.

```

	Query Match	2.6%	Score 122	DB 1	Length 1196	
	Similarity	20.4%	Pred. No. 0.54			
	Matches	178	Conservative 113	Mismatches 333	Indels 248	Gaps 43
QY	114	LTGSGFSLTSPDSBPTVTTGQGLSS-----AGGVNLENIR	151			
DB	14	LEFFFFPSLSPFASPSQSLYREIHQILSPKDYLPDKNLLPDWSSNKPCTPFGVTCRDXK	73			
QY	152	KLVAVGNFETADGGAIKGASFLITGTGSPALPSNNS-----SSTKGAIATPAGARIAN	205			
DB	74	VTSIDLSKPLNVGSAVSSLSLTGLSLTFLSNHNGSVSGFKCSALTSLDIRRS	133			
QY	206	NTGYVRFLSNINASTSGAIDDEGTSILSNKKFLYPEGNAKTTGGAICNTKASGPELLI	265			
DB	134	LSGPVTTTLTSLSCSG-----LKFLLVNSN-----	158			
QY	266	SNKKTLIPASNVAFETSGGAIIHAKKALLASGSGPTFELRNWVSSATPKGAISIDAGSELST	325			
DB	159	-----TLDFGKX---SGG-----LKLNSLEVLVDLSANSISGANVVGWLS--DGCEELH	204			

```

/ APPLICANT: McAnultfe, Olivia
/ APPLICANT: Perill, Andrea Accarate
/ TITLE OF INVENTION: Nucleic Acid Sequences Encoding
/ TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
/ FILE REFERENCE: 5051-694
/ CURRENT APPLICATION NUMBER: US/11/074,176
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: 60/551,161
/ PRIOR FILING DATE: 2004-03-08
/ NUMBER OF SEQ. ID NOS: 381
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ. ID NO 12
/
/ LENGTH: 457
/ TYPE: PRT
/ ORGANISM: Lactobacillus acidophilus
US-11-074-176-12

Query Match      2.5%; Score 119.5; DB 7; Length 457;
Best Local Similarity 19.7%; Freq. No. 0.22;

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:20:23 ; Search time 108.724 Seconds
(without alignments)
3750.264 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 928
Sequence: 1 MKTSIPWLVSSVLAFFSCHL.....MELRGSSRYNVDTKLRP 928

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	928	100.0	928	2	AAW88417 Chlamydia
2	928	100.0	928	3	AAW88417 Chlamydia
3	928	100.0	928	5	ABW90583 Chlamydia
4	928	100.0	928	6	ABW90583 Chlamydia
5	827	89.1	949	2	AAW35060 Chlamydia
6	12	1.3	230	2	AAW34612 Chlamydia
7	12	1.3	746	5	ABW90535 Chlamydia
8	12	1.3	928	2	AAW88421 Chlamydia
9	12	1.3	928	3	AAW94327 Chlamydia
10	10	1.1	10	7	ADW30988 HLA bindi
11	10	1.1	10	7	ADW30926 HLA bindi
12	10	1.1	10	7	ADW30940 HLA bindi
13	10	1.1	395	5	ABW90536 Chlamydia
14	10	1.1	450	5	ABW94617 Chlamydia
15	10	1.1	839	5	ABW56002 Chlamydia
16	10	1.1	839	5	ABW98211 Chlamydia
17	10	1.1	839	6	ABW62627 C. psittaci
18	10	1.1	945	2	AAW88428 Chlamydia
19	10	1.1	945	3	AAW63368 Amino aci
20	9	1.0	9	7	ADW30943 HLA bindi
21	9	1.0	930	2	AAW88424 Chlamydia
22	9	1.0	930	2	AAW35052 Chlamydia
23	9	1.0	930	5	AAW90240 Chlamydia
24	9	1.0	930	5	ABW90548 Chlamydia

25	9	1.0	930	6	ABU26756 Protein e
26	8	0.9	76	8	ADK48420 Streptoco
27	8	0.9	76	8	ADR94994 Novel S.
28	8	0.9	76	9	AEA58864 Streptoco
29	8	0.9	93	4	AAU14380 Human nov
30	8	0.9	93	4	AAU14144 Human nov
31	8	0.9	93	8	ADH80698 Human pol
32	8	0.9	112	4	AAW74946 Human col
33	8	0.9	199	8	ADL05508 M. catarr
34	8	0.9	218	3	AAW95842 Maize hea
35	8	0.9	218	4	AAW82764 Maize hea
36	8	0.9	218	7	ABU10034 Maize mil
37	8	0.9	218	8	ADW48273 Polypepti
38	8	0.9	227	8	ADH51632 Novel hum
39	8	0.9	234	4	AAW87249 Novel cen
40	8	0.9	234	8	ADL54564 Novel hum
41	8	0.9	251	7	ADP59589 Human pol
42	8	0.9	267	4	AAU19709 Human nov
43	8	0.9	267	5	ABP47929 Human pol
44	8	0.9	267	7	ADC10891 Human ext
45	8	0.9	312	8	ADY12178 Plant ful

ALIGNMENTS

RESULT 1.
ID AAW88417 standard, protein; 928 AA.
AC AAW88417;
XX
DT 17-OCT-2003 (revised)
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp4.
XX
KM Omp4, outer membrane protein 4; surface exposed protein; antigen;
infection; diagnosis; vaccine; atherosclerosis; asthma.
XX
OS Chlamydia pneumoniae.
XX
PN W09858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WC-DK000266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHR/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
WPI: 1999-105610/09.
DR N-PSDB; AAX06816.
XX
PT Species-specific test for identifying mammals infected with Chlamydia
pneumoniae - comprises detecting antibodies specific for outer membrane
proteins of C. pneumoniae or nucleic acids encoding these proteins.
XX
PS Claim 7; Page 40-42; 115pp; English.
XX
CC This polypeptide comprises the novel 98.9 kDa surface exposed protein
Omp4 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
acid sequence was deduced from DNA (see AAX06816) isolated from a C.
pneumoniae expression library. The invention provides 12 novel surface
exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid
sequences encoding them (see AAX06816-27). A new species specific test is
claimed that is used to identify mammals (including humans) infected with
Chlamydia pneumoniae. The test comprises detecting antibodies specific
for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer

CC membrane proteins, especially by PCR. The proteins are also used in the
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
 CC proteins can also be used in the immunization of mammals, the nucleic
 CC acids being particularly useful as DNA vaccines for effecting in vivo
 CC expression of antigens. The vaccines may also prevent atherosclerosis and
 CC bronchial asthma, which are possibly associated with C. pneumoniae.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX
 SQ Sequence 928 AA;

Query Match 100.0%; Score 928; DB 2; Length 928;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSLPVLVSVYAFSCCHLSLANEELSPDPSFNGNINSGFTPTKTSATYTSLTGDFV 60
 DB 1 MKTSLPVLVSVYAFSCCHLSLANEELSPDPSFNGNINSGFTPTKTSATYTSLTGDFV 60
 QY 61 FYERKGTPLSDSCFKQTTDLNLFNGHSLTFGFDAGTHAGAASTANKULTFSGFS 120
 DB 61 FYERKGTPLSDSCFKQTTDLNLFNGHSLTFGFDAGTHAGAASTANKULTFSGFS 120
 QY 121 LLSFDSPTSTVTTGGTSSAGVNLNTRKLVVAGNFTADGAIKASFLITGSGD 180
 DB 121 LLSFDSPTSTVTTGGTSSAGVNLNTRKLVVAGNFTADGAIKASFLITGSGD 180
 QY 181 ALFENNSSSTKGAIAATTAGARINNTGYVFLSNIASTSGAIDDEGTSILSNKFLYF 240
 DB 181 ALFENNSSSTKGAIAATTAGARINNTGYVFLSNIASTSGAIDDEGTSILSNKFLYF 240
 QY 241 EGNNAKTGGAICTKASGSPELLISNNKTLIFASNAVETSGAIIHAKKALSSGGTFEF 300
 DB 241 EGNNAKTGGAICTKASGSPELLISNNKTLIFASNAVETSGAIIHAKKALSSGGTFEF 300
 QY 301 LRNNVSATPKGAIISIDAGSELSSAETGNITFVRNLTLTGSTDTPKRNAINIGSNGK 360
 DB 301 LRNNVSATPKGAIISIDAGSELSSAETGNITFVRNLTLTGSTDTPKRNAINIGSNGK 360
 QY 361 FTFLRAKNNHTIFYDPTSEGTSSDYLKINNSAGALNPQGITLFSGETLTDELKVA 420
 DB 361 FTFLRAKNNHTIFYDPTSEGTSSDYLKINNSAGALNPQGITLFSGETLTDELKVA 420
 QY 421 DNLSKSFQTPVSLSGKLLLOKGVLTLESTSFSGEAGSLLGMDSGTTLSTTAGSITITNLG 480
 DB 421 DNLSKSFQTPVSLSGKLLLOKGVLTLESTSFSGEAGSLLGMDSGTTLSTTAGSITITNLG 480
 QY 481 INVDLSLGIKOPVSLTAKGASNKVIVSGKLNLDIEGNITESHMSHOLFSLLKITVDAD 540
 DB 481 INVDLSLGIKOPVSLTAKGASNKVIVSGKLNLDIEGNITESHMSHOLFSLLKITVDAD 540
 QY 541 VDTNVDLSLIPVAEDPNSRYGQGNVMTTDTATNTKEATATWTGTGFPVSPERKS 600
 DB 541 VDTNVDLSLIPVAEDPNSRYGQGNVMTTDTATNTKEATATWTGTGFPVSPERKS 600
 QY 601 ALVNCNTLWGVTFDIRSLQQLVEIGATGMEHQFGWSSMTNPLHKTGDENRKGFRHTSGG 660
 DB 601 ALVNCNTLWGVTFDIRSLQQLVEIGATGMEHQFGWSSMTNPLHKTGDENRKGFRHTSGG 660
 QY 661 YVIGGSATPKDDLPFTAFCHLPADKCCFPAHNSRRTYGGTLFPKSHHTLOPQNYRLG 720
 DB 661 YVIGGSATPKDDLPFTAFCHLPADKCCFPAHNSRRTYGGTLFPKSHHTLOPQNYRLG 720
 QY 721 RAKSESSEIEKFPREIPLALDVQVSFSDNRMETHTYSLSESEGSWNECIAGIGIDL 780
 DB 721 RAKSESSEIEKFPREIPLALDVQVSFSDNRMETHTYSLSESEGSWNECIAGIGIDL 780
 QY 781 PFVLSNPAPLFTKFTLPQMKVEMVYVVSQNSPFESSSDGSGFSGIGRLNLSPVGAKFYVGD 840
 DB 781 PFVLSNPAPLFTKFTLPQMKVEMVYVVSQNSPFESSSDGSGFSGIGRLNLSPVGAKFYVGD 840
 QY 841 IGDSTYDLSGFPFVSDVYRRNPQSTATLYMSPDKIKIGUNLSROAFLLRGSNNYVYNSN 900
 DB 841 IGDSTYDLSGFPFVSDVYRRNPQSTATLYMSPDKIKIGUNLSROAFLLRGSNNYVYNSN 900

QY 901 CELFGHYAMELRGSSRNRYVDVGTKLRF 928
 DB 901 CELFGHYAMELRGSSRNRYVDVGTKLRF 928

RESULT 2

AAAY90236
 ID AAAY90236 standard; protein; 928 AA.

XX
 AC AAAY90236;

XX 12-SEP-2003 (revised)
 DT 29-AUG-2000 (first entry)

XX Chlamydia antigen CPN100634.

KM Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
 KW therapy; upper respiratory tract disease; bronchitis; sinusitis;
 KM asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.

OS Chlamydia pneumoniae.

PN W0200032794-A2.

PD 08-JUN-2000.

PF 01-DEC-1999; 99WO-CA001147.

XX 01-DEC-1998; 98US-0110339P.

PR 01-DEC-1998; 98US-0110340P.

PR 01-DEC-1998; 98US-0110427P.

PR 01-DEC-1998; 98US-0110428P.

XX (CONN-) CONNAUGHT LAB LTD.

XX Mordin AD, Oomen RP, Wang J;

DR WPI; 2000-412339/35.

DR N-PADB; AAA30847, AAA30848.

XX Claim 16; Fig 1; 174p; English.

XX This sequence is a Chlamydia antigen of the invention, designated

CC CPN100634. The nucleic acids (and their complementary sequences) may be

CC used as diagnostic agents for detecting the presence of nucleic acids

CC encoding Chlamydia antigens in samples according to standard methods, and

CC therefore, for diagnosing Chlamydia infections. For example, they may be

CC used as primers and probes for diagnostic polymerase chain reaction (PCR)

CC assays. Antisense sequences may be used to down regulate expression of

CC the proteins and may be used to treat infections. The nucleic acids may

CC also be used to produce the protein antigens they encode according to

CC standard recombinant DNA methodologies. The proteins may then be used as

CC antigens for the production of antibodies (i.e. as vaccines) for

CC preventing infection by Chlamydia. The antibodies may also be used as

CC diagnostic reagents for detecting infections. Chlamydia is a pathogen

CC implicated in the development of (for example) community acquired

CC pneumonia, upper respiratory tract disease (especially bronchitis and

CC sinusitis, asthmatic bronchitis, adult-onset asthma and acute

OS field)

SQ Sequence 928 AA;

Query Match 100.0%; Score 928; DB 3; Length 928;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSLIPWLVSVYLAFCCHLQSLANBELSPDDSFNGNIDSGTFPTPKTSATYSLTGDFV 60
 DB 1 MKTSLIPWLVSVYLAFCCHLQSLANBELSPDDSFNGNIDSGTFPTPKTSATYSLTGDFV 60
 QY 61 FYRPGKTPSLDSCFKQKTNDLTFGLNGHSLTFQGFIDAGHAGAASTANKULTFSGFS 120
 DB 61 FYRPGKTPSLDSCFKQKTNDLTFGLNGHSLTFQGFIDAGHAGAASTANKULTFSGFS 120
 QY 121 LLSFDDSPSTVTYTGQGLSSAGVNLNRLKLVGNFSTAGGAIKGSFLLTGSGD 180
 DB 121 LLSFDDSPSTVTYTGQGLSSAGVNLNRLKLVGNFSTAGGAIKGSFLLTGSGD 180
 QY 181 ALFSNNSSSTKGAIAATTAGARIANTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
 DB 181 ALFSNNSSSTKGAIAATTAGARIANTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
 QY 241 EGNAAKTGGALCNTKASGSPPELLISNNKTLIFASNAETSGAIIHAKKLALSSGGTFEF 300
 DB 241 EGNAAKTGGALCNTKASGSPPELLISNNKTLIFASNAETSGAIIHAKKLALSSGGTFEF 300
 QY 301 LRNNVSATPKGALISTDASGELSLAETGNITFVRNLTLTGSGTDPKRNAINIGSNGK 360
 DB 301 LRNNVSATPKGALISTDASGELSLAETGNITFVRNLTLTGSGTDPKRNAINIGSNGK 360
 QY 361 FTELRAKNTTIFFYDPTTSEGTSDVLKINNAGALNPYOGTILFSGETLTADELKVA 420
 DB 361 FTELRAKNTTIFFYDPTTSEGTSDVLKINNAGALNPYOGTILFSGETLTADELKVA 420
 QY 421 DNLKSFQTPVSLSGCKLLQKGVLTLESTPSOBSGLLMDSGTLLSTTAGSIITTNLG 480
 DB 421 DNLKSFQTPVSLSGCKLLQKGVLTLESTPSOBSGLLMDSGTLLSTTAGSIITTNLG 480
 QY 481 INVDSLGKQPVSLTAKGANKYIVSGKLLIDEGIVSHMFSDQLFSLKITYDAD 540
 DB 481 INVDSLGKQPVSLTAKGANKYIVSGKLLIDEGIVSHMFSDQLFSLKITYDAD 540
 QY 541 VDTNVDISLIPVAEDPNSEYGFQOGMNMTTDTATNKEATATWTKTGPVSPERKS 600
 DB 541 VDTNVDISLIPVAEDPNSEYGFQOGMNMTTDTATNKEATATWTKTGPVSPERKS 600
 QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNPLAKTGDENRKGFRTSGG 660
 DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNPLAKTGDENRKGFRTSGG 660
 QY 661 YVIGGSAMTKDULFTFAFGHLFARDKDCFIANNHSTTYGTLFPRKSHTLQPNYLRIG 720
 DB 661 YVIGGSAMTKDULFTFAFGHLFARDKDCFIANNHSTTYGTLFPRKSHTLQPNYLRIG 720
 QY 721 RAKFSBAIKKPREIPLALDVQVFSHSDNRMEHTHTSLPESFGSMNSCIIAGGIGLDL 780
 DB 721 RAKFSBAIKKPREIPLALDVQVFSHSDNRMEHTHTSLPESFGSMNSCIIAGGIGLDL 780
 QY 781 PFVLSNHPFLKFTFIPQMKVEMVYVSONSFESSSDRGFSIRGLNLSIPVAKFVQGD 840
 DB 781 PFVLSNHPFLKFTFIPQMKVEMVYVSONSFESSSDRGFSIRGLNLSIPVAKFVQGD 840
 QY 841 IGSYTYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGNLSBOAFLRGSNNTYNSN 900
 DB 841 IGSYTYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGNLSBOAFLRGSNNTYNSN 900
 QY 901 CELFGHAMELRGSSRYNYDVGTKLRF 928
 DB 901 CELFGHAMELRGSSRYNYDVGTKLRF 928

RESULT 3
 ABB90583
 ID ABB90583 standard; protein: 928 AA.
 AC ABB90583;
 XX
 DT 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)
 XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
 DE Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
 XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
 KW Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CML029.
 XX Chlamydia pneumoniae.
 OS Chlamydia pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT Protein /label= Signal_peptide
 FT 18..928
 FT /note= "mature protein"
 XX
 PN MO200202606-A2.
 XX
 PD 10-JAN-2002.
 XX
 PE 03-JUL-2001; 2001WO-1B001445.
 XX
 PR 03-JUL-2000; 2000GB-00016363.
 PR 11-JUL-2000; 2000GB-00017047.
 PR 21-JUL-2000; 2000GB-00017983.
 PR 07-AUG-2000; 2000GB-00019368.
 PR 18-AUG-2000; 2000GB-00020440.
 PR 14-SEP-2000; 2000GB-00022583.
 PR 10-NOV-2000; 2000GB-00027549.
 PR 22-DEC-2000; 2000GB-00031706.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Ratti G, Grandi G;
 DR N-PSDB; ABL91241.
 XX
 DR WPI; 2002-154726/20.
 XX
 PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
 XX
 PS Claim 1; Page 96-97; 364pp; English.
 XX
 CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed Chlamydia pneumoniae protein of the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 928 AA;

Query Match 100.0%; Score 928; DB 5; Length 928;
 Best local similarity 100.0%; Pred. No. 0;
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTSLIPWLVSVYLAFCCHLQSLANBELSPDDSFNGNIDSGTFPTPKTSATYSLTGDFV 60
 DB 1 MKTSLIPWLVSVYLAFCCHLQSLANBELSPDDSFNGNIDSGTFPTPKTSATYSLTGDFV 60

```

QY 61 FYEFGKGTPLSDSCFKOTTDNLTFGLNGHSLTFGIDAGTAGAAGTAANKLTFSGFS 120
DB 61 FYEFGKGTPLSDSCFKOTTDNLTFGLNGHSLTFGIDAGTAGAAGTAANKLTFSGFS 120
QY 121 LLSFDSSTPTVTYTGQGTLLSAGGVNLENIRKLVAAGNFSTADGAIKGAFLITGSGD 180
DB 121 LLSFDSSTPTVTYTGQGTLLSAGGVNLENIRKLVAAGNFSTADGAIKGAFLITGSGD 180
QY 181 ALFENNSSSTKGAIATTAGARINANGYVRFNLINASTSGAIDDEGTSILSNKKELYP 240
DB 181 ALFENNSSSTKGAIATTAGARINANGYVRFNLINASTSGAIDDEGTSILSNKKELYP 240
QY 241 EGNAAKTGGAICTTKASGSEPELLIISNNKTLIFASNAFETSGAIIHAKKALSSGGEFTEF 300
DB 241 EGNAAKTGGAICTTKASGSEPELLIISNNKTLIFASNAFETSGAIIHAKKALSSGGEFTEF 300
QY 301 LRRNVSSATPKGAIISIDAGSELISAEFGNITFVRNLTLTGSGTDPKRNAINIGSNGK 360
DB 301 LRRNVSSATPKGAIISIDAGSELISAEFGNITFVRNLTLTGSGTDPKRNAINIGSNGK 360
QY 361 FTELRAAKNHTIFPYDPTISSEGTSDVAKINNGSAGALNPQGTILFSGEITLADDELKVA 420
DB 361 FTELRAAKNHTIFPYDPTISSEGTSDVAKINNGSAGALNPQGTILFSGEITLADDELKVA 420
QY 421 DNLKSSFTQPVSLSGGKLLQKGYLTSESTSFQSEAGSLGMDSGTLLSTTAGSITITNLG 480
DB 421 DNLKSSFTQPVSLSGGKLLQKGYLTSESTSFQSEAGSLGMDSGTLLSTTAGSITITNLG 480
QY 481 INVDSLGLKQVSLTAKASNKVIVSGKLNLDIEGNIEYSHMSHQDLFSLIKITVDAD 540
DB 481 INVDSLGLKQVSLTAKASNKVIVSGKLNLDIEGNIEYSHMSHQDLFSLIKITVDAD 540
QY 541 VDTNWDISLLPVPAEDPNSEYFGQGNVMTDTATNTKEATATMTKGFVSPERKS 600
DB 541 VDTNWDISLLPVPAEDPNSEYFGQGNVMTDTATNTKEATATMTKGFVSPERKS 600
QY 601 ALVCTNLGVTFTDRLSLQOLVEIGATGMEHKQGFVSSMTNFKLKTGDENRKGRHRTSGG 660
DB 601 ALVCTNLGVTFTDRLSLQOLVEIGATGMEHKQGFVSSMTNFKLKTGDENRKGRHRTSGG 660
QY 661 YVIGGSAHTPKDLDLTFAPFCHLPARDKOCFLAHNNSRTYGGTLTFKSHSLTOPNYRLG 720
DB 661 YVIGGSAHTPKDLDLTFAPFCHLPARDKOCFLAHNNSRTYGGTLTFKSHSLTOPNYRLG 720
QY 721 RAKTESAIEKPRRIPLALDVQVSFSDNRMETHYSLPESBSGWSNECIIAGGIGDL 780
DB 721 RAKTESAIEKPRRIPLALDVQVSFSDNRMETHYSLPESBSGWSNECIIAGGIGDL 780
QY 781 PFVLSPNPPLFKTFIPQMKVEMVYVSSQNSPFESSSDGGRGFSIGRLNLISIPVGAKEVQGD 840
DB 781 PFVLSPNPPLFKTFIPQMKVEMVYVSSQNSPFESSSDGGRGFSIGRLNLISIPVGAKEVQGD 840
QY 841 IGDSTYTLISGFVSDVYRNPNQSTATLVMSPDSWKIRGNLSRQAFLLRGSNNVYNSN 900
DB 841 IGDSTYTLISGFVSDVYRNPNQSTATLVMSPDSWKIRGNLSRQAFLLRGSNNVYNSN 900
QY 901 CELFGHYAMELRGSSRNVDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNVDVGTCLRF 928

```

RESULT 4
 ABU26757
 ID ABU26757 standard; protein; 928 AA.
 AC ABU26757;
 XX
 DT 23-OCT-2003 (revised)
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #12284.
 XX

```

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Chlamydia pneumoniae.
XX
PN NC020027.183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002MO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zykind JW,
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI: 2003-029926/02.
DR N-PSDB; ACA30627.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 54681; 1766bp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway of
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 928 AA;

```

Query Match 100.0%; Score 928; DB 6; Length 928;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKTSPWLVSVYAFSCHLQSLANEELSPDPSFNGNIDSGFTPTKATYATSLTGDVF 60
DB 1 MKTSPWLVSVYAFSCHLQSLANEELSPDPSFNGNIDSGFTPTKATYATSLTGDVF 60

```

```
QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFSGFS 120
DB 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFSGFS 120
QY 121 LLSFDSSTPTVTTGGTTLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGSGD 180
DB 121 LLSFDSSTPTVTTGGTTLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGSGD 180
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSLISNNKFLYF 240
DB 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSLISNNKFLYF 240
QY 241 EGNAAKTTGGAI CNTKASGSPPELLISNNKTLIFASVNAETSGAIIHAKKALASSGFTTF 300
DB 241 EGNAAKTTGGAI CNTKASGSPPELLISNNKTLIFASVNAETSGAIIHAKKALASSGFTTF 300
QY 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFRNTLTGSGTDPKRNAINIGSNGK 360
DB 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFRNTLTGSGTDPKRNAINIGSNGK 360
QY 361 FTFLRAAKNHTIFFYDPIITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
DB 361 FTFLRAAKNHTIFFYDPIITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNLKSSFTQPVSLSGGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 480
DB 421 DNLKSSFTQPVSLSGGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 480
QY 481 INVDISLQKQPVSLTAKGASNKYIVSGKMLIDIEGNIYSSNMFSDQLFSLKITVDAD 540
DB 481 INVDISLQKQPVSLTAKGASNKYIVSGKMLIDIEGNIYSSNMFSDQLFSLKITVDAD 540
QY 541 VDNVNDISLIPVPAEPNSEYGFQGOVMNMTTDTATNKATATWTKGFVSPERKS 600
DB 541 VDNVNDISLIPVPAEPNSEYGFQGOVMNMTTDTATNKATATWTKGFVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNPLHKTGDENRKGFRTSGG 660
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNPLHKTGDENRKGFRTSGG 660
QY 661 YVIGGSAHTPKDILFTFAFCHLPARDKOCITAHNNSTTYGTLFPKASHILOPONTIRLG 720
DB 661 YVIGGSAHTPKDILFTFAFCHLPARDKOCITAHNNSTTYGTLFPKASHILOPONTIRLG 720
QY 721 RAKPSESATKEKPREIPLALDVQVFSHSNRMETHYTSLPESGGSNNTCIAGIGLIL 780
DB 721 RAKPSESATKEKPREIPLALDVQVFSHSNRMETHYTSLPESGGSNNTCIAGIGLIL 780
QY 781 PFVLSNHPLEKTFIIPQMKVEMVYVQNSFESSSDRGFSIGRLNLMSIPVGAKEVQGD 840
DB 781 PFVLSNHPLEKTFIIPQMKVEMVYVQNSFESSSDRGFSIGRLNLMSIPVGAKEVQGD 840
QY 841 IGDSTYDLSGFVSDVYRNNPOSTATLVMSPDWKIRGNLSRQAFLLRGNNVYNSN 900
DB 841 IGDSTYDLSGFVSDVYRNNPOSTATLVMSPDWKIRGNLSRQAFLLRGNNVYNSN 900
QY 901 CELFGHAMELRGSSRYNDVGTKLF 928
DB 901 CELFGHAMELRGSSRYNDVGTKLF 928

RESULT 5
ID AAY35060 standard; protein: 949 AA.
XX AAY35060;
XX 17-OCT-2003 (revised)
XX 13-SEP-1999 (first entry)
DE Chlamydia pneumoniae cellular envelope protein.
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
```

```
KW sinuinitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KM neutralising epitope.
OS Chlamydia pneumoniae.
XX MO927105-A2.
XX 03-JUN-1999.
XX 20-NOV-1998; 98MO-1B001890.
XX 21-NOV-1997; 97PR-00014673.
XX 04-NOV-1998; 980S-0107078P.
XX (GEST ) GENSET.
XX Griffais R;
XX WPI; 1999-357842/30.
XX Genome sequence of Chlamydia pneumoniae.
PS Page 947-949; Disclosure: 1912pp; English.
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 949 AA;
Query Match 89.1%; Score 827; DB 2; Length 949;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKTSLPVLVSSVLAFSCHLQSLANEELLSPDSEFNGNIDSGTFPKTSATYSLTGDF 60
DB 22 MKTSLPVLVSSVLAFSCHLQSLANEELLSPDSEFNGNIDSGTFPKTSATYSLTGDF 81
QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFSGFS 120
DB 82 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFSGFS 141
QY 121 LLSFDSSTPTVTTGGTTLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGSGD 180
DB 142 LLSFDSSTPTVTTGGTTLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGSGD 201
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSLISNNKFLYF 240
DB 202 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSLISNNKFLYF 261
QY 241 EGNAAKTTGGAI CNTKASGSPPELLISNNKTLIFASVNAETSGAIIHAKKALASSGFTTF 300
DB 262 EGNAAKTTGGAI CNTKASGSPPELLISNNKTLIFASVNAETSGAIIHAKKALASSGFTTF 321
QY 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFRNTLTGSGTDPKRNAINIGSNGK 360
DB 322 LRNNVSSATPKGGAISIDASGELSLSAETGNITFRNTLTGSGTDPKRNAINIGSNGK 381
QY 361 FTFLRAAKNHTIFFYDPIITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
DB 382 FTFLRAAKNHTIFFYDPIITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 441
QY 421 DNLKSSFTQPVSLSGGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 480
DB 442 DNLKSSFTQPVSLSGGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 501
```

```

QY 481 INVDSLGKQPVSTLAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITVDAD 540
D 502 INVDSLGKQPVSTLAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITVDAD 561
QY 541 VDTNVDISSLIPVAEDPNSSEYFGQGMNVMTDTATNTKEATATYTKTGFPVSPERKS 600
D 562 VDTNVDISSLIPVAEDPNSSEYFGQGMNVMTDTATNTKEATATYTKTGFPVSPERKS 621
QY 601 ALVNCNTLWGVFTDRLSLQQLVEIGATGMEHKQGFVWSMTNPLFKTGDENRKGFRTSGG 660
D 622 ALVNCNTLWGVFTDRLSLQQLVEIGATGMEHKQGFVWSMTNPLFKTGDENRKGFRTSGG 681
QY 661 YVIGSANTPKODLFTFAFCHLFARDKDCFTAHNNSRTYGGTLFPKSHHTLQPNYLRIG 720
D 682 YVIGSANTPKODLFTFAFCHLFARDKDCFTAHNNSRTYGGTLFPKSHHTLQPNYLRIG 741
QY 721 RAKFSESAIEKFPREIPLALDVQVSFHSNDRMETHYSLPESGSGSNCEIAGIGIDL 780
D 742 RAKFSESAIEKFPREIPLALDVQVSFHSNDRMETHYSLPESGSGSNCEIAGIGIDL 801
QY 781 PFVLSNPHPLFKFTLPQMKVEMVYVYVSONSFESSSDGSGFISGRLLNLSTIPVGAKFVQGD 840
D 802 PFVLSNPHPLFKFTLPQMKVEMVYVYVSONSFESSSDGSGFISGRLLNLSTIPVGAKFVQGD 861
QY 841 IGDSTTYDLSGFPVSDVYRNPNPOSTATLLWSPDSWKLKRGNLRSQAFLLRGSNNVYVNSN 900
D 862 IGDSTTYDLSGFPVSDVYRNPNPOSTATLLWSPDSWKLKRGNLRSQAFLLRGSNNVYVNSN 921
QY 901 CELFGHYAMELRGSSRNYNVDVGTKLRF 928
D 922 CELFGHYAMELRGSSRNYNVDVGTKLRF 949

RESULT 6
AAV34612
ID AAV34612 standard; protein; 230 AA.
AC AAV34612;
XX
XX 17-OCT-2003 (revised)
DT 13-SEP-1999 (first entry)
XX
XX Chlamydia pneumoniae transmembrane protein sequence.
DE
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX MO9927105-A2.
PN
XX 03-JUN-1999.
PD
XX 20-NOV-1998; 98WO-IB001890.
PF
XX 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
XX (GSEST ) GENSET.
PA
XX Grifffais R;
PI
XX WPI, 1999-357842/30.
DR
XX
XX Genome sequence of Chlamydia pneumoniae.
PT
XX Page 633; Disclosure; 1912pp; English.
PS
XX
XX AAV34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAV3190) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis

```

```

CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAV34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 230 AA:
Query Match 1.3%; Score 12; DB 2; Length 230;
Best Local Similarity 100.0%; Pred.No. 0.019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 910 ELRGSSRNYNVD 921
D 212 ELRGSSRNYNVD 223

RESULT 7
ABB90535
ID ABB90535 standard; protein; 746 AA.
AC ABB90535;
XX
XX 29-AUG-2003 (revised)
DT 29-JUL-2002 (first entry)
XX
DE Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.
XX
XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KM human respiratory disease; cardiovascular disease; atherosclerosis;
KM coronary artery disease; carotid artery stenosis; myocardial infarction;
KM cerebrovascular disease; aortic aneurysm; claudication; stroke;
KM strain CWL029.
XX
XX Chlamydia pneumoniae.
OS
XX MO200202606-A2.
PN
XX 10-JAN-2002.
PD
XX
XX 03-JUL-2001; 2001WO-IB001445.
PF
XX 03-JUL-2000; 2000GB-00016363.
PR 11-JUL-2000; 2000GB-00017047.
XX 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
XX 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
XX 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
XX
XX (CHIR-) CHIRON SPA.
PA
XX Ratti G, Grandi G;
PI
XX WPI: 2002-154726/20.
DR N-PSDB; ABL91193.
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
XX Claim 1; Page 49-50; 364pp; English.
PS
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as

```

CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed Chlamydia pneumoniae protein of the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 746 AA;

Query Match 1.3%; Score 12; DB 5; Length 746;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921
 DB 728 ELRGSSRNRYND 739

RESULT 8
 ID AAW88421 standard; protein; 928 AA.
 XX AAW88421;

AC AAW88421;
 DT 17-OCT-2003 (revised)
 DT 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp8.

DE Omp8; outer membrane protein 8; surface exposed protein; antigen;
 KM infection; diagnosis; vaccine; atherosclerosis; asthma.

XX Chlamydia pneumoniae.

OS WO958953-A2.

XX 30-DEC-1998.

PF 19-JUN-1998; 98MO-DK000266.

XX 23-JUN-1997; 97DK-00000744.

PA (BIRK/) BIRKELUND S.
 PA (CHRI/) CHRISTIANSEN G.

PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

XX WPI, 1999-105610/09.

DR N-PSDB; AAX06820.

XX Species-specific test for identifying mammals infected with Chlamydia
 PT pneumoniae - comprises detecting antibodies specific for outer membrane
 PT proteins of C. pneumoniae or nucleic acids encoding these proteins.

XX Claim 7, Page 53-55, 115pp; English.

XX This polypeptide comprises the novel 90.0 kDa surface exposed protein
 CC Omp8 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
 CC acid sequence was deduced from DNA (see AAX06820) isolated from a C.
 CC pneumoniae expression library. The invention provides 12 novel surface
 CC exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid
 CC sequences encoding them (see AAX06816-27). A new species specific test is
 CC claimed that is used to identify mammals (including humans) infected with
 CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
 CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used in the
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
 CC proteins can also be used in the immunization of mammals, the nucleic

CC acids being particularly useful as DNA vaccines for effecting in vivo
 CC expression of antigens. The vaccines may also prevent atherosclerosis and
 CC bronchial asthma, which are possibly associated with C. pneumoniae.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 928 AA;

Query Match 1.3%; Score 12; DB 2; Length 928;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921
 DB 910 ELRGSSRNRYND 921

RESULT 9
 ID AAY94327 standard; protein; 928 AA.
 XX AAY94327;

AC AAY94327;
 DT 12-SEP-2003 (revised)
 DT 11-AUG-2000 (first entry)

XX Chlamydia pneumoniae 98kD putative outer membrane protein.

XX Chlamydia; antigen; vaccine; infection; outer membrane protein.

XX Chlamydia pneumoniae.

PN WO200026237-A2.

XX 11-MAY-2000.

PF 29-OCT-1999; 99MO-GB003579.

XX 29-OCT-1998; 98US-0106070P.

PR 01-MAR-1999; 99US-0122066P.

PR 27-OCT-1999; 99US-00428122.

PA (CONN-) CONNAUGHT LAB LTD.

PI Murdin AD, Oomen RP, Dunn PL;

XX WPI, 2000-365569/31.

DR N-PSDB; AAA27021.

XX Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for
 PT vaccination and protection against Chlamydia infection.

XX Claim 6; Fig 1; 93pp; English.

XX The present sequence is the 98kDa putative outer membrane protein from
 CC Chlamydia pneumoniae. The genomic sequence was amplified using two PCR
 CC primers. The 5' primer contains a NotI restriction site, a ribosome
 CC binding site, an initiation codon and a sequence close to the 5' end of
 CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
 CC contains the sequence encoding the C-terminal sequence of the putative
 CC outer membrane protein and a BglI restriction site. The stop codon was
 CC excluded and an additional nucleotide was inserted to obtain an in-frame
 CC C-terminal fusion with the Histidine tag. The PCR product was cloned into
 CC a eukaryotic expression vector (pCA-Myc-His) by restricting both the
 CC vector and the PCR product with NotI and BamHI and performing a ligation
 CC reaction. This expression vector was injected intramuscularly and
 CC intranasally into mice, which were subsequently inoculated with Chlamydia
 CC pneumoniae. The chlamydial lung titers of the immunised mice were lower
 CC than those of the controls. Thus the 98kDa putative outer membrane
 CC protein can be used as a vaccine to provide protection against Chlamydia
 CC infections, especially Chlamydia pneumoniae infections. The present
 CC polypeptide may also be administered orally to treat Chlamydia infection.
 CC (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 928 AA;

Query Match 1.3%; Score 12; DB 3; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 910 ELRGSSRNRYND 921
|||
910 ELRGSSRNRYND 921

RESULT 10

ADW30988

ID ADW30988 standard; peptide; 10 AA.

AC ADW30988;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #1738.

XX Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KM viral disease; cancer.

XX Unidentified.

OS WO2003040165-A2.

PN 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PA Sette A, Sidney J, Southwood S;

PI WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 10 AA;

Query Match 1.1%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 528 QLFSLKITY 537

Db 1 QLFSLKITY 10
|||||

RESULT 11

ADW30926

ID ADW30926 standard; peptide; 10 AA.

AC ADW30926;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #1676.

XX Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KM viral disease; cancer.

XX Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PA Sette A, Sidney J, Southwood S;

PI WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 10 AA;

Query Match 1.1%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 601 ALVNCNTLMGV 610
|||||

Db 1 ALVNCNTLMGV 10

RESULT 12

ADW30940

ID ADW30940 standard; peptide; 10 AA.

XX	ADW303940;
AC	
XX	
DT	10-MAR-2005 (first entry)
XX	
DE	HLA binding epitope #1690.
XX	
KW	Vincutide; cyrostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW	MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW	vital disease; cancer.
XX	
OS	Unidentified.
PN	
XX	WO2003040165-A2.
XX	
PD	15-MAY-2003.
XX	
PF	18-OCT-2001; 2001WO-US051650.
XX	
PR	19-OCT-2000; 2000US-0242350P.
PR	20-APR-2001; 2001US-0285624P.
PA	(EPIM-) EPIMMUNE INC.
PI	Sette A, Sidney J, Southwood S;
XX	
DR	WPI; 2003-441519/41.
XX	
PT	New composition comprising at least one peptide having allele-specific
PT	binding motifs for HLA, useful for preventing, treating or diagnosing
PT	vital diseases and cancer.
XX	
PS	Claim 1; Page 52-379; 382pp; English.
XX	
CC	The invention relates to a composition comprising at least one peptide
CC	having an isolated, prepared epitope selected from any of the sequences
CC	from 30 lists given in the specification. Also disclosed is a method for
CC	inducing a cytotoxic T cell response against a pre-selected antigen in a
CC	patient expressing a specific MHC class I allele by contacting cytotoxic
CC	T cells from the patient with the composition cited above. The
CC	composition comprises an epitope that is joined by an amino acid linker.
CC	The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC	bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC	-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC	binds to a complex of the HLA molecule and the epitope. Specifically
CC	claimed are peptides having allele-specific binding motifs for HLA. The
CC	compositions and methods are useful for preventing, treating or
CC	diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC	diagnostic agents for evaluating immune responses, for making antibodies
CC	and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
CC	ADW37745 represent epitopes of the invention as given in Tables 2-31.
XX	
SQ	Sequence 10 AA;
OY	887 FLRGSNNTV 896
	FLRGSNNTV 10
Db	
	Query Match 1.1%; Score 10; DB 7; Length 10;
	Best Local Similarity 100.0%; Pred. No. 0.1;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 13	
ABB90536	
ID	ABB90536 standard; protein; 395 AA.
XX	
AC	ABB90536;
XX	
DT	29-AUG-2003 (revised)
DT	29-JUL-2002 (first entry)
XX	
DE	Chlamydia pneumoniae cp0019 protein, SEQ ID NO:21.

XX Chlamydia infection; antigen; immunogen; vaccine; diagnosis;
KM human respiratory disease; cardiovascular disease; atherosclerosis;
KM coronary artery disease; carotid artery stenosis; myocardial infarction;
KM cerebrovascular disease; aortic aneurysm; claudication; stroke;
XX strain CML029.
OS Chlamydephila pneumoniae.
PN WO200202606-A2.
PD 10-JAN-2002.
XX
XX
PF 03-JUL-2001; 2001WO-IB001445.
XX
XX 03-JUL-2000; 2000GB-00016363.
PR 11-JUL-2000; 2000GB-00017047.
PR 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
PR 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
PR 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX Ratti G, Grandi G;
PI
XX
XX WPI; 2002-154726/20.
DR N-PsDB; ABL91194.
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PI preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
XX
PS Claim 1; Page 51; 364pp; English.
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed Chlamydia pneumoniae protein of the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
SQ Sequence 395 AA:

Query Match 1.1%; Score 10; DB 5; Length 395;
Best Local Similarity 100.0%; Pred. No. 2.8; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNYY 919
DB 377 ELRGSSRNYY 386

RESULT 14
ID AAY34617
NC AAY34617; standard; protein; 450 AA.
XX
XX AAY34617;
DT 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)
 XX Chlamydia pneumoniae transmembrane protein sequence.
 DE
 XX Respiratory disease: pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KM neutralising epitope.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae.
 XX
 PS Page 637-638; Disclosure; 1912pp; English.
 XX
 CC AAY3484-Y35879 represent the proteins encoded by all the open reading
 CC frames in the complete genome (see AAY9190) of Chlamydia pneumoniae. C.
 CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
 CC and is thought to be a contributing factor in heart disease, sarcoidosis,
 CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
 CC polypeptides encoded by the open reading frames of the C. pneumoniae
 CC genome (see AAY3484-Y35879) can be used in immunogenic compositions as
 CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
 CC be used as immunogenic compositions, especially where the vector directs
 CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
 CC -OCT-2003 to standardise OS field)
 XX
 SQ Sequence 450 AA;
 Query Match 1.1%; Score 10; DB 2; Length 450;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 910 ELRGSSRNYN 919
 Db 432 ELRGSSRNYN 441
 RESULT 15
 ABP56002
 ID ABP56002 standard; protein; 839 AA.
 XX
 AC ABP56002;
 XX
 DT 29-AUG-2003 (revised)
 DT 25-FEB-2003 (first entry)
 XX
 DE Chlamydia psittaci antigen CP4#4 protein SEQ ID NO:23.
 XX
 KW Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
 KM immunisation; antibacterial; infection.
 XX
 OS Chlamydia psittaci.
 XX
 PN WO200253588-A2.
 PD 11-JUL-2002.
 XX
 PF 17-DEC-2001; 2001WO-US048715.

XX
 PR 15-DEC-2000; 2000US-00738269.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B;
 XX
 DR WPI; 2002-537942/57.
 DR N-PADB; ABC04758.
 XX
 PT Vaccine for immunization of animal, preferably bovine, against Chlamydia
 PT psittaci, comprises at least one polynucleotide having a C. psittaci
 PT sequence, or at least one C. psittaci antigen.
 XX
 PS Claim 9; Page 127-129; 164pp; English.
 XX
 CC The present invention describes a vaccine (I) for the immunisation of an
 CC animal against Chlamydia psittaci comprising at least one polynucleotide
 CC (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
 CC (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
 CC useful for the immunisation of a bovine. The present sequence represents
 CC a C. psittaci antigen from the present invention. (Updated on 29-AUG-2003
 CC to standardise OS field)
 XX
 SQ Sequence 839 AA;
 Query Match 1.1%; Score 10; DB 5; Length 839;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 79 TDNLTFILGNG 88
 Db 81 TDNLTFILGNG 90
 Search completed: November 25, 2005, 14:37:12
 Job time : 116.724 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:22:05 ; Search time 24.3603 Seconds
(without alignments)
3665.352 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 928

Sequence: 1 MKTSIPWLVVSSVLAFSCHL.....MEIRGSSRMNVVDVTKLRF 928

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	928	100.0	928	2 D72077	polymorphic outer
2	928	100.0	928	2 H86546	polymorphic outer
3	928	100.0	949	2 F81591	polymorphic membra
4	12	1.3	772	2 H86492	Pmp_3 [imported] -
5	10	1.1	445	2 E86493	Pmp_5 [imported] -
6	9	1.0	261	2 F82795	hypothetical prote
7	9	1.0	737	2 S55117	probable membrane
8	9	1.0	930	2 D86546	polymorphic outer
9	9	1.0	930	2 D72078	polymorphic outer
10	9	1.0	930	2 A81591	polymorphic membra
11	8	0.9	218	2 T01412	heat shock protein
12	8	0.9	241	2 H82072	DNA repair protein
13	8	0.9	342	2 S75783	dtbD_lucase 4.6-de
14	8	0.9	391	2 S06969	pectate lyase (EC
15	8	0.9	406	1 UC5041	fosmidomycin resis
16	8	0.9	406	2 H85545	fosmidomycin resis
17	8	0.9	406	2 D90695	fosmidomycin resis
18	8	0.9	427	2 A86493	polymorphic outer
19	8	0.9	445	2 AD2023	carboxyl-terminal
20	8	0.9	466	2 B69842	probable oxidoredu
21	8	0.9	469	2 T52659	sulfate adenylylitr
22	8	0.9	711	2 S43464	ecdysteroid-induce
23	8	0.9	922	2 F81539	polymorphic membra
24	8	0.9	922	2 B72131	polymorphic outer
25	8	0.9	922	2 H86491	polymorphic outer
26	8	0.9	928	2 G86546	polymorphic outer
27	8	0.9	928	2 G81591	polymorphic membra
28	8	0.9	973	2 B86547	polymorphic outer
29	8	0.9	973	2 F72076	polymorphic outer

30	8	0.9	995	2 C81593	polymorphic membra
31	8	0.9	1013	2 G71460	probable outer mem
32	8	0.9	1276	2 B86546	polymorphic outer
33	8	0.9	1276	2 C81591	polymorphic membra
34	8	0.9	1407	2 B72078	polymorphic outer
35	8	0.9	1723	2 H86557	polymorphic membra
36	8	0.9	1723	2 E72067	polymorphic membra
37	8	0.9	1732	2 C81601	polymorphic membra
38	7	0.8	42	2 I51291	aldolase C - chick
39	7	0.8	43	2 A35771	dnak-type molecula
40	7	0.8	56	2 S46471	IG heavy chain V-r
41	7	0.8	78	2 S46461	IG heavy chain V r
42	7	0.8	81	2 B81133	hypothetical prote
43	7	0.8	91	1 EPR2	phospholipid trans
44	7	0.8	96	2 S26923	IG heavy chain V r
45	7	0.8	96	2 S26924	IG heavy chain V r

ALIGNMENTS

RESULT 1

D72077 polymorphic outer membrane protein g family - Chlamydomydia pneumoniae (strain CWL029)

C:Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae

C:date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: D72077

R:Kalmun, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:reference number: A72000; WUID:9920606; PMID:10192388

A:Accession: D72077

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-928 <ARN>

A:Cross-references: UNIPROT:086164; UNIPARC:UPI000002FFEF; GB:AE001628; GB:AE001363; NID:

A:Experimental source: strain CWL029

C:Genetics:

A:Gene: pmp_11

C:superfamily: Chlamydomydia pneumoniae polymorphic outer membrane protein G

Query Match	100.0%	Score 928;	DB 2;	Length 928;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches	928;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MKTSIPWLVVSSVLAFSCHLQSLANBELISPPDSFNGNIDSGTFPPKTSATYSLTGDF	60	
DB	1	MKTSIPWLVVSSVLAFSCHLQSLANBELISPPDSFNGNIDSGTFPPKTSATYSLTGDF	60	
QY	61	FTEPGKGTPLSDSCFQQTNDNLTFIENGHSLTFEGFIADGTHAGAAASTYANKNLFPESGFS	120	
DB	61	FTEPGKGTPLSDSCFQQTNDNLTFIENGHSLTFEGFIADGTHAGAAASTYANKNLFPESGFS	120	
QY	121	LISFDSFSTVTYTGGLTSSAGVNLLENIRKLVVAGNFSTADGAIKAGASFLTGTSGD	180	
DB	121	LISFDSFSTVTYTGGLTSSAGVNLLENIRKLVVAGNFSTADGAIKAGASFLTGTSGD	180	
QY	181	ALPSSNNSSTKGAIAATTGARIANNVTGVRFLSNIASSGAIIDDEGSIISNNKFLYF	240	
DB	181	ALPSSNNSSTKGAIAATTGARIANNVTGVRFLSNIASSGAIIDDEGSIISNNKFLYF	240	
QY	241	EGNAAKTTGCAICNTKASGPELIISNNKTLIFASVNAETSGAIIHAKKALLSSGGFTTF	300	
DB	241	EGNAAKTTGCAICNTKASGPELIISNNKTLIFASVNAETSGAIIHAKKALLSSGGFTTF	300	
QY	301	LNNVSSATPKGGAISIDAGELSLAETGNTTFVRNLTITTTGSDTDPKRNAINIGSNCK	360	
DB	301	LNNVSSATPKGGAISIDAGELSLAETGNTTFVRNLTITTTGSDTDPKRNAINIGSNCK	360	
QY	361	FTELRAAKNHTIFPDPTISBEGTSSDVLLKINNGAGALNPYGGTILFSGETTLTADELKVA	420	
DB	361	FTELRAAKNHTIFPDPTISBEGTSSDVLLKINNGAGALNPYGGTILFSGETTLTADELKVA	420	

QY 421 DNLSKSFQPVSLSGKLLQKGVLTLESTFSQEAAGLLGMDSGTLLTAGSITITNLG 480
DB 421 DNLSKSFQPVSLSGKLLQKGVLTLESTFSQEAAGLLGMDSGTLLTAGSITITNLG 480
QY 481 INVDLSGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540
DB 481 INVDLSGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540
QY 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMVNMVTTDTATNTKEATATWTKGFPVSPERKS 600
DB 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMVNMVTTDTATNTKEATATWTKGFPVSPERKS 600
QY 601 ALVCNTLMGVFTDRLSIQQLVEIGATGMEHKQGFWSMTNPLHKTGDENRKGFRHTSGG 660
DB 601 ALVCNTLMGVFTDRLSIQQLVEIGATGMEHKQGFWSMTNPLHKTGDENRKGFRHTSGG 660
QY 661 YVIGGSATTPKODLFTFAFCHLFPARDKCFIAHNSRTYGGTLFFKXSHTLQPNYLRIG 720
DB 661 YVIGGSATTPKODLFTFAFCHLFPARDKCFIAHNSRTYGGTLFFKXSHTLQPNYLRIG 720
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLGLD 780
DB 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLGLD 780
QY 781 PVLNSNHPHLPKFTPIQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840
DB 781 PVLNSNHPHLPKFTPIQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840
QY 841 IGDSTYDLSGFPVSDVYRNPNQSTATLVMSPDWKIRGSLRSQAFLLRGSNNVYNSN 900
DB 841 IGDSTYDLSGFPVSDVYRNPNQSTATLVMSPDWKIRGSLRSQAFLLRGSNNVYNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 2

H86546
polymorphic outer membrane protein G family [imported] - Chlamydia pneumoniae (strat)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86546
R:Strain: M.; Hiraoka, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; PMID:20330349; PMID:10871362
A:Accession: H86546
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-928 <STO>
A:Cross-references: UNIPROT:O86164; UNIPARC:UPI000002FFBF; GB:BA000008; NID:g8978822; PT
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_11
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 928; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTSLPWLVSVSLAFSCHLSLANBELSPDPSFNGNIDSGTTPPKTSATTVSLTGVF 60
DB 1 MKTSLPWLVSVSLAFSCHLSLANBELSPDPSFNGNIDSGTTPPKTSATTVSLTGVF 60
QY 61 FYEPKGPPLSDCKKOTTDNLTFLGNGHSLTFGTIDAGTAGAASLTANKNLTFSGFS 120
DB 61 FYEPKGPPLSDCKKOTTDNLTFLGNGHSLTFGTIDAGTAGAASLTANKNLTFSGFS 120
QY 121 LISPSSSTTYTTCOGTLLSSAGVNLNIRKLVVAGNPSRADGAIIGASFLTLGTNSGD 180
DB 121 LISPSSSTTYTTCOGTLLSSAGVNLNIRKLVVAGNPSRADGAIIGASFLTLGTNSGD 180

QY 181 ALFSSNNSSTKGAIALTTAGARIANNNTGYVRLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 181 ALFSSNNSSTKGAIALTTAGARIANNNTGYVRLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAATTGALCNTAAGSSPELLISNNKTLFASVVAATSGAIIHAKKALAISSGFTEF 300
DB 241 EGNAAATTGALCNTAAGSSPELLISNNKTLFASVVAATSGAIIHAKKALAISSGFTEF 300
QY 301 LRNNSSATPKGGAISIDASGELSLAETGNITFVANTLTGTTGSDTTPKRNAINIGSNK 360
DB 301 LRNNSSATPKGGAISIDASGELSLAETGNITFVANTLTGTTGSDTTPKRNAINIGSNK 360
QY 361 FTELRAKNTHTFFYDPTISEGTSVDVLKINNGSAGALNPYQGTILFSGETLTADLKYA 420
DB 361 FTELRAKNTHTFFYDPTISEGTSVDVLKINNGSAGALNPYQGTILFSGETLTADLKYA 420
QY 421 DNLSKSFQPVSLSGKLLQKGVLTLESTFSQEAAGLLGMDSGTLLTAGSITITNLG 480
DB 421 DNLSKSFQPVSLSGKLLQKGVLTLESTFSQEAAGLLGMDSGTLLTAGSITITNLG 480
QY 481 INVDLSGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540
DB 481 INVDLSGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540
QY 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMVNMVTTDTATNTKEATATWTKGFPVSPERKS 600
DB 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMVNMVTTDTATNTKEATATWTKGFPVSPERKS 600
QY 601 ALVCNTLMGVFTDRLSIQQLVEIGATGMEHKQGFWSMTNPLHKTGDENRKGFRHTSGG 660
DB 601 ALVCNTLMGVFTDRLSIQQLVEIGATGMEHKQGFWSMTNPLHKTGDENRKGFRHTSGG 660
QY 661 YVIGGSATTPKODLFTFAFCHLFPARDKCFIAHNSRTYGGTLFFKXSHTLQPNYLRIG 720
DB 661 YVIGGSATTPKODLFTFAFCHLFPARDKCFIAHNSRTYGGTLFFKXSHTLQPNYLRIG 720
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLGLD 780
DB 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLGLD 780
QY 781 PVLNSNHPHLPKFTPIQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840
DB 781 PVLNSNHPHLPKFTPIQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840
QY 841 IGDSTYDLSGFPVSDVYRNPNQSTATLVMSPDWKIRGSLRSQAFLLRGSNNVYNSN 900
DB 841 IGDSTYDLSGFPVSDVYRNPNQSTATLVMSPDWKIRGSLRSQAFLLRGSNNVYNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 3

F81591
polymorphic membrane protein G family CP0302 [imported] - Chlamydia pneumoniae (strat)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C:Accession: F81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; PMID:20150255; PMID:10684935
A:Accession: F81591
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-949 <REA>
A:Cross-references: UNIPARC:UPI00001655FA; GB:AE002192; GB:AE002161; NID:g7189226; PIDN:
A:Experimental source: strain AR39, HU cells
C:Genetics:
A:Gene: CP0302
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 928; DB 2; Length 949;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSIWLVSIVLAFSCHLQSLANBELLSPPDSFNGNIDSGTFPTKATSYSLTGDF 60
 DB 22 MKTSIWLVSIVLAFSCHLQSLANBELLSPPDSFNGNIDSGTFPTKATSYSLTGDF 81
 QY 61 FYRPGKTPIDSCFQOTDNLTFPLNGHSLTFGFIADGHAAGAATSTANKULTSGFS 120
 DB 82 FYRPGKTPIDSCFQOTDNLTFPLNGHSLTFGFIADGHAAGAATSTANKULTSGFS 141
 QY 121 LLSFDSPTTVTYTGCGTSLSSAGVNLNIRKLVAGNFSTADGAIKGAFLITGSGD 180
 DB 142 LLSFDSPTTVTYTGCGTSLSSAGVNLNIRKLVAGNFSTADGAIKGAFLITGSGD 201
 QY 181 ALFSNNSSSTKGAIAATTAGARIANNITGVYRPLSNIASTSGAIDDEGSIISNNKFLYF 240
 DB 202 ALFSNNSSSTKGAIAATTAGARIANNITGVYRPLSNIASTSGAIDDEGSIISNNKFLYF 261
 QY 241 EGNAAATTGGAICNTAKASGPELIIISNNKTLIFASNAVAETSGAIIAKKALSSGGTF 300
 DB 262 EGNAAATTGGAICNTAKASGPELIIISNNKTLIFASNAVAETSGAIIAKKALSSGGTF 321
 QY 301 LRNNSSATPKGGAISIDAGSELISAEIGNITFVRNTLTGTTGTDTPKNAINIGNGK 360
 DB 322 LRNNSSATPKGGAISIDAGSELISAEIGNITFVRNTLTGTTGTDTPKNAINIGNGK 381
 QY 361 FTFLRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNYOGTILFSGETTLADELKA 420
 DB 382 FTFLRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNYOGTILFSGETTLADELKA 441
 QY 421 DNKSSFTQVSLSSGGTLLQKVTLESTFSQDAGSLCMBDGTTLSTAGSITTTNIG 480
 DB 442 DNKSSFTQVSLSSGGTLLQKVTLESTFSQDAGSLCMBDGTTLSTAGSITTTNIG 501
 QY 481 INVDSLKQPVSLTAKGANKYIVSGKLNLDIEGIVESHMFSDQLFSLKITVDAD 540
 DB 502 INVDSLKQPVSLTAKGANKYIVSGKLNLDIEGIVESHMFSDQLFSLKITVDAD 561
 QY 541 VDTNVDISLLIPVPAEDPNSYGFQGGVNNMTTDTANTKEATATWTGTGVPSPERKS 600
 DB 562 VDTNVDISLLIPVPAEDPNSYGFQGGVNNMTTDTANTKEATATWTGTGVPSPERKS 621
 QY 601 ALVGNLWGVFTDIRSLQQLVEIGATGMEKQGFVWSMTNPLHKTGDENRKKFRHTSG 660
 DB 622 ALVGNLWGVFTDIRSLQQLVEIGATGMEKQGFVWSMTNPLHKTGDENRKKFRHTSG 681
 QY 661 YVIGGSAHPTKDDLTFPAFCHLFAKDQCFIAHNNSTYGTLPFKHSHLOPONYLRIG 720
 DB 682 YVIGGSAHPTKDDLTFPAFCHLFAKDQCFIAHNNSTYGTLPFKHSHLOPONYLRIG 741
 QY 721 RAKFSSEALEKFPREIPLALDVQVSFSDNRMETHYTSLPESGGSWNECIAGIGLDL 780
 DB 742 RAKFSSEALEKFPREIPLALDVQVSFSDNRMETHYTSLPESGGSWNECIAGIGLDL 801
 QY 781 PVLASNPPLPKTFIPQMKVEMYVVSQNSFPESSDRGSGISGLLNLSTIPVAKKFGQD 840
 DB 802 PVLASNPPLPKTFIPQMKVEMYVVSQNSFPESSDRGSGISGLLNLSTIPVAKKFGQD 861
 QY 841 IGSYTYDLSGFFVSDVYRRNPSTATLWVSPDMSKIRGNLSROAFILRGNNVYNSN 900
 DB 862 IGSYTYDLSGFFVSDVYRRNPSTATLWVSPDMSKIRGNLSROAFILRGNNVYNSN 921
 QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
 DB 922 CELFGHYAMELRGSSRNRYNDVGTCLRF 949

RESULT 4
 H86492
 Pmp_3 [imported] - Chlamydia pneumoniae (strain J138)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 09-Jul-2004
 C/Accession: H86492
 R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi
 Nucleic Acids Res. 28, 2311-2314, 2000
 A/Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
 A/Reference number: A86491; PMID:20330349; PMID:10871362
 A/Accession: H86492
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-772 <STO>
 A/Cross-references: UNIPROT:Q9RB71; UNIPARC:UPI00000CCC33; GB:BA000008; NID:98978389; PII
 A/Experimental source: strain J138
 C/Genetics:
 A/Gene: pmp_3_2

Query Match 1.3%; Score 12; DB 2; Length 772;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921
 DB 754 ELRGSSRNRYND 765

RESULT 5

H86493
 Pmp_5 [imported] - Chlamydia pneumoniae (strain J138)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 09-Jul-2004

C/Accession: H86493

R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A/Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A/Reference number: A86491; PMID:20330349; PMID:10871362

A/Accession: H86493

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-445 <STO>

A/Cross-references: UNIPROT:Q9RB67; UNIPARC:UPI00000CCC32; GB:BA000008; NID:98978394; PII

A/Experimental source: strain J138

C/Genetics:
 A/Gene: pmp_5_2

Query Match 1.1%; Score 10; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYN 919
 DB 427 ELRGSSRNRYN 436

RESULT 6

H82795
 hypothetical protein XF0515 [imported] - Xylella fastidiosa (strain 9a5c)

C/Species: Xylella fastidiosa

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #ext_change 09-Jul-2004

C/Accession: F82795

R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; PMID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A53328 below

A/Accession: F82795

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-261 <SIM>

A/Cross-references: UNIPROT:Q9PF21; UNIPARC:UPI00000C2434; GB:AE003900; GB:AE003849; NID:

A/Experimental source: strain 9a5c

R/Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al

Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canaipo, U.E.A.; Carraro, D.M.; Carreir, H.

as-Neto, B.; Docena, C.; El-Dorcy, H.; Facincani, A.P.; Ferreira, A.U.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Friaga, J.S.; Franca, S.C.; Franco, M.C.; Fromm
J.D.; Junqueira, M.L.; Kemp, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuxame, E.E.; Laizy
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A:Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, R.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0515

Query Match 1.0%; Score 9; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 LKKTVDAD 540
Db 4 LKKTVDAD 12

RESULT 7
S5117
probable membrane protein YML002w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YW8270.01; hypothetical protein YW957.17
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: S5117; S53028
R:Gentles, S.; Bowman, S.
submitted to the EMBL Data Library, June 1995
A:Reference number: S5102
A:Accession: S5117
A:Molecule type: DNA
A:Residues: 1-254 <GEN>
A:Cross-references: UNIPROT:Q04263; UNIPARC:UPI0000168AB0; EMBL:Z49810; NID:g854472; PID
A:Experimental source: strain AB972
R:Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53028
A:Accession: S53028
A:Molecule type: DNA
A:Residues: 250-737 <DEV>
A:Cross-references: UNIPARC:UPI0000168A84; EMBL:Z48613; NID:g728645; PID:g728646; MIPS:X
A:Experimental source: strain AB972
C:Genetics:
A:Map position: 13L
C:Superfamily: Saccharomyces probable membrane protein YML002w
C:Keywords: transmembrane protein
F:15-31/Domain: transmembrane #status predicted <TM>

Query Match 1.0%; Score 9; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 FSNSSSTK 191
Db 48 FSNSSSTK 56

RESULT 8
D86546
polymorphic outer membrane protein G family [imported] - Chlamydomonas reinhardtii (strai
C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C:Accession: D86546
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae U138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: D86546
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-930 <STO>
A:Cross-references: UNIPARC:UPI00001655FB; GB:BA000008; NID:g8978618; PIDN:BA098654.1; G
A:Experimental source: strain U138
C:Genetics:
A:Gene: pmp_8
C:Superfamily: Chlamydomonas pneumoniae polymorphic outer membrane protein G

Query Match 1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 AGAASSTTA 110
Db 107 AGAASSTTA 115

RESULT 9
D72078
polymorphic outer membrane protein g family - Chlamydomonas pneumoniae (strain CML029)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: D72078
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:9920606; PMID:10192388
A:Accession: D72078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-930 <AN>
A:Cross-references: UNIPROT:Q92393; UNIPARC:UPI000004708C; GB:AE001627; GB:AE001363; NID:
A:Experimental source: strain CML029
C:Genetics:
A:Gene: pmp_8
C:Superfamily: Chlamydomonas pneumoniae polymorphic outer membrane protein G

Query Match 1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 AGAASSTTA 110
Db 107 AGAASSTTA 115

RESULT 10
A81591
polymorphic membrane protein G family CP0307 [imported] - Chlamydomonas pneumoniae (strai
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoDn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: A81591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-930 <REA>
A:Cross-references: UNIPROT:Q92393; UNIPARC:UPI00001655FB; GB:AE002193; GB:AE002161; NID
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0307
C:Superfamily: Chlamydomonas pneumoniae polymorphic outer membrane protein G

Query Match 1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 AGAASSTTA 110
Db 107 AGAASSTTA 115

Db 107 AGAASTTA 115

RESULT 11

T01412
heat shock protein hsp22 precursor, mitochondrial - maize
C/Species: Zea mays (maize)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01412
R/Lund, A.A.; Blum, P.H.; Bhattacharjee, D.; Elthon, T.E.
Plant Physiol. 116, 1097-1110, 1998
A/Title: Heat-stress response of maize mitochondria.
A/Reference number: Z14320; MUID:98169424; PMID:9501143
A/Accession: T01412
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-218 <LUN>
A/Cross-references: UNIPROT:Q64960, UNIPARC:UPI00000A372C, EMBL:AF035460, NID:G3015620;
A/Experimental source: strain B73
C/Genetics:
A/Genome: hsp22
C/Superfamily: alpha-crystallin-related small heat shock protein
C/Keywords: heat shock; mitochondrion; stress-induced protein
F/1-45/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F/46-218/Product: low molecular weight heat shock protein hsp22 #status predicted <MAT>

Query Match 0.9%; Score 8; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 SIGRLNTL 828
Db 95 SIGRLNTL 102

RESULT 12

H82072
DNA repair protein Reco VC2459 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: H82072
R/Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.U.;
Charadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Basse, S.; Qin, H.; Dragol, I.; Sellers, F.
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: AB2035; MUID:20406833; PMID:10952301
A/Accession: H82072
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-241 <HEI>
A/Cross-references: UNIPROT:Q9KPB4, UNIPARC:UPI00001335B1, GB:AE004316, GB:AE003852, NID:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Genes: VC2459
A/Map position: 1
C/Superfamily: reco protein

Query Match 0.9%; Score 8; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 DNLTFIGN 87
Db 179 DNLTFIGN 186

RESULT 13

S75783
dtdpglucose 4,6-dehydratase (EC 4.2.1.46) - Synecchocystis sp. (strain PCC 6803)
C/Species: Synecchocystis sp.
A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S75783
R/Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
S.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S75783
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-342 <KAN>
A/Cross-references: UNIPROT:Q55420, UNIPARC:UPI00000D3539, EMBL:D64003, GB:AB001339; NID:
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C/Keywords: carbon-oxygen lyase; hydro-lyase
F/6-33/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 0.9%; Score 8; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 23;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 FVQGDIGD 843
Db 58 FVQGDIGD 65

RESULT 14

S06969
pectate lyase (EC 4.2.2.2) D precursor - Erwinia chrysanthemi
C/Species: Erwinia chrysanthemi
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: S06969
R/van Gijsegem, F.
Mol. Microbiol. 3, 1415-1424, 1989
A/Title: Relationship between the pel genes of the pelAAB cluster in Erwinia chrysanthemi
A/Reference number: S06968; MUID:90136069; PMID:2615652
A/Accession: S06969
A/Molecule type: DNA
A/Residues: 1-391 <GIJ>
A/Cross-references: UNIPROT:P18209, UNIPARC:UPI0000131580, EMBL:X17284; NID:G42343; PIDN:
A/Experimental source: strain B374
C/Genetics:
A/Genes: pelD
C/Superfamily: pectate lyase
C/Keywords: carbon-oxygen lyase
F/1-31/Domain: signal sequence #status predicted <SIG>
F/32-391/Product: pectate lyase D #status predicted <MAT>

Query Match 0.9%; Score 8; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 IGSNGKFT 362
Db 123 IGSNGKFT 130

RESULT 15

JCS041
foamdomycin resistance protein - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: JCS041; F64778
R/Fujisaki, S.; Ohnuma, S.; Horiuchi, T.; Takahashi, I.; Teukui, S.; Nishimura, Y.; Nishi
Gene 175, 83-87, 1996
A/Title: Cloning of a gene from Escherichia coli that confers resistance to foamdomycin
A/Reference number: JCS041; MUID:97074653; PMID:8917080
A/Accession: JCS041
A/Molecule type: DNA
A/Residues: 1-406 <FUJ>
A/Cross-references: UNIPROT:P52067, UNIPARC:UPI000012AC73, DDBJ:D73370, NID:G1019359; PII
A/Experimental source: strain DH5alpha

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64778
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-406 <BLAT>
A:Cross-references: UNIPARC:UPI000012AC73; GB:AE000154; GB:U00096; NID:G1786683; PIDN:AB
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: fsr
C:Function:
A:Description: confers resistance to fosmidomycin
C:Superfamily: fosmidomycin resistance protein
C:Keywords: antibiotic resistance; transmembrane protein
F:104-120/Domain: transmembrane #status predicted <TM1>
F:181-197/Domain: transmembrane #status predicted <TM2>
F:225-241/Domain: transmembrane #status predicted <TM3>
F:267-283/Domain: transmembrane #status predicted <TM4>
F:294-310/Domain: transmembrane #status predicted <TM5>
F:320-336/Domain: transmembrane #status predicted <TM6>
F:358-374/Domain: transmembrane #status predicted <TM7>
F:381-397/Domain: transmembrane #status predicted <TM8>

Query Match 0.9%; Score 8; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 102 AGAASSTT 109
|||
Db 11 AGAASSTT 18

Search completed: November 25, 2005, 14:48:09
Job time : 31.3603 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:21:48 ; Search time 141.29 Seconds
(without alignments)
4633.951 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 928
Sequence: 1 MKTSLPWLVSVAFLAFSCHL.....MEIRGSSRNRYVDVGTKLRF 928

Scoring table: OLIGO
Gapop 60.0 , Gapect 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	928	100.0	928	1	PMP11_CHLPN
2	14	1.5	1024	2	OS16J7_CHLAB
3	12	1.3	649	2	P71134_CHLAB
4	12	1.3	772	2	O9R871_CHLBN
5	12	1.3	1378	2	O516J2_CHLAB
6	10	1.1	252	2	O8V1H7_CHLAB
7	10	1.1	445	2	O7VQ99_CHLBN
8	10	1.1	445	2	O9RB67_CHLBN
9	10	1.1	839	2	P77792_CHLAB
10	9	1.0	261	2	O9P8Z1_XYLPA
11	9	1.0	337	2	O7NH75_GLOVT
12	9	1.0	475	2	O6W3N9_9PROT
13	9	1.0	737	1	YMA2_YEAST
14	9	1.0	737	2	O6B2L5_YEAST
15	9	1.0	868	2	O823X4_CHICV
16	9	1.0	930	1	PMP8_CHLBN
17	8	0.9	47	2	O87267_SIVCZ
18	8	0.9	51	2	O87187_SIVCZ
19	8	0.9	51	2	O87191_SIVCZ
20	8	0.9	51	2	O87203_SIVCZ
21	8	0.9	51	2	O87213_SIVCZ
22	8	0.9	51	2	O87263_SIVCZ
23	8	0.9	51	2	O87270_SIVCZ
24	8	0.9	56	2	O4S2C4_TETNG
25	8	0.9	93	2	O7PX31_ANOGA
26	8	0.9	112	2	O76812_ANOGA
27	8	0.9	132	2	O61516_ANOGA
28	8	0.9	132	2	O6Q1B7_PLOIN
29	8	0.9	139	2	O7YR19_PIG
30	8	0.9	139	2	O7YR11_PIG
31	8	0.9	143	2	P79123_BOVIN

32	8	0.9	165	2	O8D7T9_VIBVU	O8d7t9 vibrio vuln
33	8	0.9	168	2	O6MFA6_PARUM	O6mfa6 parachlamyd
34	8	0.9	174	2	O88Y02_LACPL	O88y02 lactobacill
35	8	0.9	182	2	O841V9_CAMEF	O841v9 campylobact
36	8	0.9	209	2	O8ENP4_OCEIH	O8enf4 oceanobacti
37	8	0.9	212	2	O7NEV3_VIBVY	O7nev3 vibrio vuln
38	8	0.9	215	2	O4UGL2_THEAN	O4ugl2 thelletia a
39	8	0.9	218	2	O64960_MAIZE	O64960 zea mays (m
40	8	0.9	227	2	O7S772_NEUCR	O7s772 neurospora
41	8	0.9	241	1	RECO_VIBCH	O9kpb4 vibrio chol
42	8	0.9	243	1	RECO_VIBPA	O87lp1 vibrio para
43	8	0.9	243	1	RECO_VIBVU	O8dc74 vibrio vuln
44	8	0.9	243	1	RECO_VIBVY	O7mp0 vibrio vuln
45	8	0.9	282	2	O61LT7_DROME	O61lt7 drosophila

ALIGNMENTS

RESULT 1
PMP11_CHLPN STANDARD: PRT: 928 AA.
ID EMP11_CHLPN
AC O86164; O9K299; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 47, Last annotation update)
DE Probable outer membrane protein pmp11 precursor (Polymorphic membrane protein 11) (outer membrane protein 4).
GN Name=pmp11; Synonyms=omp4; OrderedLocustName=Cp00449, CP0302, CPB0468;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.
OX NCBI_TaxId=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CWL029 / VR1310;
RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
RT membrane proteins of Chlamydia pneumoniae.";
RL Infect. Immun. 67:375-383 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CWL029 / VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495 (1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CWL029;
RX MEDLINE=9920606; PubMed=10192388; DOI=10.1038/7716;
RA Kalman S., Mitchell W.P., Marathe R., Lamell C.J., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Ueteyback T.R., Berry K.J.,
RA Baas S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwaltin W.L., Nelson W.C., Deboy R.T., Kolonay J.F.,
RA McClary G., Salzberg S.L., Eisen J.A., Frazer C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=U138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;

```

RA Shira'i M., Hiraikawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA."
RT Nucleic Acids Res. 28:2311-2314(2000) .
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] .
RC STRAIN-TW-183;
RA Geng M.M., Schumacher A., Muehldorfer I., Benach K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Welchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis."
RL submitted (May-2002) to the EMBL/Genbank/DBJ databases.
CC -1 SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
CC (Potential) .
CC -1 SIMILARITY: Belongs to the PMP outer membrane protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ001311; CA04672.1; -; Genomic DNA.
CC EMBL; AJ133034; CAB37072.1; -; Genomic DNA.
CC EMBL; AE001628; AAD18593.1; -; Genomic DNA.
CC EMBL; AE002197; AAF38159.1; ALT_INIT; Genomic_DNA.
CC EMBL; BA000008; BAA98658.1; -; Genomic_DNA.
CC EMBL; AE017158; AAP98399.1; -; Genomic_DNA.
CC PIR; D72077; D72077.
CC PIR; H86546; H86546.
CC PHC1-2DPAGE; O86164; -.
CC TIGR; CP0302; -.
DR InterPro; IPR005546; Auto_transpbeta.
DR InterPro; IPR011427; ChlamPMP_M.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlam_PMP; 6.
DR Pfam; PF07548; ChlamPMP_M; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 5.
DR Complete proteome; Membrane; MultiGene family; Outer membrane; Signal.
KW SIGNAL
FT SIGNAL 1 24 Potential.
FT CHAIN 25 928 Probable outer membrane protein pmp1.
SQ SEQUENCE 928 AA; 98904 MW; 788BCDD62C911402 CRC64;

Query Match 100.0%; Score 928; DB 1; Length 928;
Match Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSLPWLVSVLAFSCHLOSLABEELLSPDPSFNGNIDSGTFPPKTSATYSLTGDF 60
DB 1 MKTSLPWLVSVLAFSCHLOSLABEELLSPDPSFNGNIDSGTFPPKTSATYSLTGDF 60
QY 61 FYEPGKGPPLSDSCFKQTTNDLFTFGNGHSLTFGFIADGTHAGAAASTTANRNLTFSGS 120
DB 61 FYEPGKGPPLSDSCFKQTTNDLFTFGNGHSLTFGFIADGTHAGAAASTTANRNLTFSGS 120
QY 61 FYEPGKGPPLSDSCFKQTTNDLFTFGNGHSLTFGFIADGTHAGAAASTTANRNLTFSGS 120
DB 61 FYEPGKGPPLSDSCFKQTTNDLFTFGNGHSLTFGFIADGTHAGAAASTTANRNLTFSGS 120
QY 121 LLSFSSSPPTVTTTQGTLSAGCVNLEIRKLVVAGNSTDGGAIKASFLTLGTSGD 180
DB 121 LLSFSSSPPTVTTTQGTLSAGCVNLEIRKLVVAGNSTDGGAIKASFLTLGTSGD 180
QY 121 LLSFSSSPPTVTTTQGTLSAGCVNLEIRKLVVAGNSTDGGAIKASFLTLGTSGD 180
DB 121 LLSFSSSPPTVTTTQGTLSAGCVNLEIRKLVVAGNSTDGGAIKASFLTLGTSGD 180
QY 181 ALFSNNSSSTKCGAIAATTGARIANTTGAVRFSLNIASTSGAIDDEGSIISNNKFLYF 240
DB 181 ALFSNNSSSTKCGAIAATTGARIANTTGAVRFSLNIASTSGAIDDEGSIISNNKFLYF 240
QY 241 EGNAAKTGGAICNTKASGSPELIISNNKTLIFASVVAETSGAIIHAKKLLASGGTFEF 300
DB 241 EGNAAKTGGAICNTKASGSPELIISNNKTLIFASVVAETSGAIIHAKKLLASGGTFEF 300
QY 301 LANNVSAATPKGGAISIDASGELSLAETGNTTTPVANTLTGSGDTPPRNAINTGSGNK 360
DB 301 LANNVSAATPKGGAISIDASGELSLAETGNTTTPVANTLTGSGDTPPRNAINTGSGNK 360
QY 301 LANNVSAATPKGGAISIDASGELSLAETGNTTTPVANTLTGSGDTPPRNAINTGSGNK 360
DB 301 LANNVSAATPKGGAISIDASGELSLAETGNTTTPVANTLTGSGDTPPRNAINTGSGNK 360

```

QY	361	TEELRAAKNHTIIFVADPITISEGTSDDVAKINNGSGALANPYOGTLLFSEETLTADELKVA	420
Db	361	FTELRAAKNHTIIFYDPITISBETSDVLKINNGSGALANPYOGTLLFSEETLTADELKVA	420
QY	421	DNLKSSFTQPSYLSGGKLLLOKGVLTBETSPFQZAGSLGMDSGTLLSTAGSITITNLG	480
Db	421	DNLKSSFTQPSYLSGGKLLLOKGVLTBETSPFQZAGSLGMDSGTLLSTAGSITITNLG	480
QY	481	INVDLSLGKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDHQLFSLKITTVDAD	540
Db	481	INVDLSLGKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDHQLFSLKITTVDAD	540
QY	541	VDINVDISLLVPVPAEDPNSEXFGQGMNVMTTDTATNYKEATATWTGTGVPSPERKS	600
Db	541	VDINVDISLLVPVPAEDPNSEXFGQGMNVMTTDTATNYKEATATWTGTGVPSPERKS	600
QY	601	ALVCTNLGVFTDIRSLQOLVEIGATGMBKQGFVWSSMTNLELHKTGDENRKGFRHTSGG	660
Db	601	ALVCTNLGVFTDIRSLQOLVEIGATGMBKQGFVWSSMTNLELHKTGDENRKGFRHTSGG	660
QY	661	YVIGGSATTPKDDLTFTFAPCHLPADKOCFLAHNNSRTYGGTLFRKSHITLOPONTLRLG	720
Db	661	YVIGGSATTPKDDLTFTFAPCHLPADKOCFLAHNNSRTYGGTLFRKSHITLOPONTLRLG	720
QY	721	RAKFSESAIEKPRRIPLALDVQVFSFSNDNMETHYSLPESSEGSWSNECIAGGIGLDL	780
Db	721	RAKFSESAIEKPRRIPLALDVQVFSFSNDNMETHYSLPESSEGSWSNECIAGGIGLDL	780
QY	781	PFLVLSNPPLPFTFLPQMKVEMVYVYSONSPFESSDDGRFSGIRLLNLISIPVGAKEVQGD	840
Db	781	PFLVLSNPPLPFTFLPQMKVEMVYVYSONSPFESSDDGRFSGIRLLNLISIPVGAKEVQGD	840
QY	841	IGDSYTYDLSCGFVUSDVYRNNPQSTATLYMSDMSKIRGNLSRQAFLLRGSNNTYNNNS	900
Db	841	IGDSYTYDLSCGFVUSDVYRNNPQSTATLYMSDMSKIRGNLSRQAFLLRGSNNTYNNNS	900
QY	901	CELFGHYAMELRGSSRNNTVDGTLKRF 928	
Db	901	CELFGHYAMELRGSSRNNTVDGTLKRF 928	

```

RESULT 2
ID      OS6L67_CHLAB PRELIMINARY;          PRT; 1024 AA.
AC      OS6L67_
DT      01-FEB-2005 (TREMBlRel. 29, Created)
DT      01-FEB-2005 (TREMBlRel. 29, Last sequence update)
DE      01-FEB-2005 (TREMBlRel. 29, Last annotation update)
DE      Polymorphic outer membrane protein.
GN      Name=pmp7G; OrderedlocusNames=CAB269;
OS      Chlamydophila abortus.
OC      Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX      NCBI_TaxId=83555;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=S26/3;
RX      PubMed=15637807; DOI=10.1101/gr.3684805;
RA      Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,
RA      Livingston M., Cerdano-Tarraga A.-M., Harris B., Doggett J.,
RA      Ormond D., Mungall K., Clarke K., Feltwell T., Hance Z., Sanders M.,
RA      Quail M.A., Plice C., Barrall B.G., Parkhill J., Lombotom D.;
RT      "The Chlamydophila abortus genome sequence reveals an array of
RT      variable proteins that contribute to interspecies variation.";
RL      Genome Res. 15:629-640(2005) .
KW      EMBL; CR848038; CAH63725.1; -; Genomic DNA.
KW      Complete proteome.
SQ      SEQUENCE 1024 AA; 108663 MW; 268B61415C8FD434 CR654;

Query Match          1.5%; Score 14; DB 2; Length 1024;
Best Local Similarity 100.0%; Prod. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      585 ATWTKTGFVPSPER 598

```

Db 702 ATWTKGFVSPSPR 715

RESULT 3

P71134.CHLAB PRELIMINARY; PRT; 649 AA.
 AC P71134;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative outer membrane protein (Fragment).
 OS Chlamydia abortus.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83555;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.,
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U72499; AAB18187.1; -; Genomic DNA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR011427; ChlamPMP_M.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 1.
 DR TIGRfam; TIGR01414; autotrans_bar1; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 649 AA; 70091 MW; 13747C68066A7F50 CRC64;

Query Match 1.3%; Score 12; DB 2; Length 649;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSRRNYND 921
 Db 631 ELRGSRRNYND 642

RESULT 4

Q9RB71.CHLPN PRELIMINARY; PRT; 772 AA.
 AC Q9RB71; Q7BX22;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Pmp_3 (Outer membrane protein 5).
 GN Name=pmp_3.2; OrderedlocusNames=CpB0018;
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83558;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=2030349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and Cw1029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TW-183;
 RA Geng M.M., Schumacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 other Chlamydia strains based on whole genome sequence analysis.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BA000008; BAA98226.1; -; Genomic DNA.
 DR EMBL; AE017157; AAP97951.1; -; Genomic DNA.
 DR PIR; H86492; H86492.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR006315; Autotransporter.

DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR011427; ChlamPMP_M.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 1.
 DR Pfam; PF02415; Chlam_PMP; 6.
 DR TIGRfam; TIGR01414; autotrans_bar1; 1.
 DR TIGRfam; TIGR01376; POMP repeat; 6.
 SQ SEQUENCE 772 AA; 82931 MW; 484FC56D635801EB CRC64;

Query Match 1.3%; Score 12; DB 2; Length 772;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSRRNYND 921
 Db 754 ELRGSRRNYND 765

RESULT 5

Q5L6J2.CHLAB PRELIMINARY; PRT; 1378 AA.
 AC Q5L6J2;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Polymorphic outer membrane protein.
 GN Name=pmp15G; Synonyms=pomp145A; OrderedlocusNames=CMB283;
 OS Chlamydia abortus.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83555;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=826/3;
 RX PubMed=15837807; DOI=10.1101/gr.3684805;
 RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,
 RA Livingstone M., Cerdeno-Tarraga A.-M., Harris B., Doggett J.,
 RA Ormond D., Mungall K., Clarke K., Felwell T., Hance Z., Sanders M.,
 RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.,
 RT "The Chlamydia abortus genome sequence reveals an array of
 RT variable proteins that contribute to interspecies variation.";
 RL Genome Res. 15:629-640(2005).
 DR EMBL; CR848038; CAH63733.1; -; Genomic DNA.
 KW Complete proteome.

QY 910 ELRGSRRNYND 921
 Db 1360 ELRGSRRNYND 1371

Query Match 1.3%; Score 12; DB 2; Length 1378;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSRRNYND 921
 Db 1360 ELRGSRRNYND 1371

RESULT 6

Q8VHT7.CHLPN PRELIMINARY; PRT; 252 AA.
 AC Q8VHT7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative polymorphic membrane protein (Fragment).
 OS Chlamydia psittaci (Chlamydia psittaci).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83554;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LLG, and POS;
 RA Laroucau K., Souriau A., Rodolakis A.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF243413; AAL36957.1; -; Genomic DNA.
 DR EMBL; AF243414; AAL36958.1; -; Genomic DNA.

DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; Chlam_PMP; 3.
 DR TIGRFAMs; TIGR01376; POMP_repatc; 3.
 FT NON TER 252
 SO SEQUENCE 252 AA; 26107 MW; 433CD4F765427318 CRC64;

Query Match 1.1%; Score 10; DB 2; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTPFLGNG 88
 DB 81 TDNLTPFLGNG 90

RESULT 7

Q7V099_CHLPPN PRELIMINARY; PRT; 445 AA.
 AC Q7V099;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Outer membrane protein 5.
 GN OrderedLocustNames=CPB0023;
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83558;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=TW-183;
 RA Geng M.M., Schuhmacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 other Chlamydia strains based on whole genome sequence analysis.";
 RI Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE017157; AA97956.1; -; Genomic_DNA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR011427; ChlamPMP M.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 SO SEQUENCE 445 AA; 49365 MW; EPA25B0C90A08AA6 CRC64;

Query Match 1.1%; Score 10; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNYN 919
 DB 427 ELRGSSRNYN 436

RESULT 8

Q9RB67_CHLPPN PRELIMINARY; PRT; 445 AA.
 AC Q9RB67;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Pmp 5.
 GN Name=pmp 5.2;
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83558;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
 RA Shirai M., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hatori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138

RT from Japan and CWL029 from USA.";
 RI Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL; BA000008; BA98231.1; -; Genomic_DNA.
 DR PIR; E86493; E86493.

DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR011427; ChlamPMP M.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.

SO SEQUENCE 445 AA; 49353 MW; EPA24AFC9C5097A6 CRC64;

Query Match 1.1%; Score 10; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNYN 919
 DB 427 ELRGSSRNYN 436

RESULT 9

P77792_CHLAB PRELIMINARY; PRT; 839 AA.
 AC P77792; Q5LSP5;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE POMP90B precursor (POMP90A precursor) (Polymorphic outer membrane
 protein).
 GN Name=pmp17g; Synonyms=pomp90B; OrderedLocustNames=CAB598;
 OS Chlamydia abortus.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83555;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=S26/3;
 RX MEDLINE=98187897; PubMed=9529048;
 RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
 RT "Molecular cloning and characterization of the genes coding for the
 highly immunogenic cluster of 90-kilodalton envelope proteins from the
 Chlamydia psittaci subtype that causes abortion in sheep.";
 RI Infect. Immun. 66:1317-1324(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=S26/3;
 RX MEDLINE=96406378; PubMed=8810511; DOI=10.1016/0378-1097(96)00281-9;
 RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
 RT "Identification of a multigene family coding for the 90 kDa proteins
 of the ovine abortion subtype of Chlamydia psittaci.";
 RI FEMS Microbiol. Lett. 142:277-281(1996).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=S26/3;
 RX PubMed=15837807; DOI=10.1101/gr.3684805;
 RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,
 RA Livingstone M., Cerdano-Tarraga A.M., Harris B., Doggett J.,
 RA Ormond D., Mungall K., Clarke K., Feltham T., Hance Z., Sanders M.,
 RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.;
 RT "The Chlamydia abortus genome sequence reveals an array of
 variable proteins that contribute to interspecies variation.";
 RI Genome Res. 15:629-640(2005).

DR EMBL; U65943; AAC15922.1; -; Genomic_DNA.
 DR EMBL; CR848038; CAH64045.1; -; Genomic_DNA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR005546; Auto_transpbeta.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR011427; ChlamPMP M.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; Chlam_PMP; 4.

DR Pfam; PF0548; ChiampM_M; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TRIPFAMs; TIGR01376; POMP_repeat; 3.
 KM Complete proteome; Signal.
 FT SIGNAL 1 16 Potential.
 CHAIN 17 839 POMP90B.
 SQ SEQUENCE 839 AA; 89825 MW; 4581C7CBAF7FFA4C4 CRC64;

Query Match 1.1%; Score 10; DB 2; Length 839;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNUTFLGNG 88
 DB 81 TDNUTFLGNG 90

RESULT 10
 Q9PFZ1_XYLFA PRELIMINARY; PRT; 261 AA.
 AC Q9PFZ1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=Xf0515;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN NUCLEOTIDE SEQUENCE.

RC STRAIN=965C;
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1098/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
 Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carriero D.M., Carter H.,
 Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 Garnier M., Goldman G.H., Goldman H.S., Gomes S.L., Gruber A.,
 Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 Krieger J.E., Kurane E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 Machado M.A., Madela A.M.B.N., Madela H.M.F., Marino C.L.,
 Marques M.V., Martins E.A.L., Martins B.M.F., Matsukuma A.Y.,
 Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Fairs A.,
 de Oliveira R.C., de Oliveira R.C., Palmieri D.A., Fairs A.,
 Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr.,
 da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 Zago M.A., Zatz M., Meidanis J., Secubal J.C.;
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
 RL Nucleic Acids Res. 31:151-159(2003).
 EMBL: AF003900; AF83325.1; -; Genomic_DNA.
 DR PIR: F82795; F82795.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 261 AA; 30007 MW; AC8E80B886D406E CRC64;

Query Match 1.0%; Score 9; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 LKITYDAD 540
 |||||

DB 4 LKITYDAD 12

RESULT 11
 Q7NHT5_GLOVI PRELIMINARY; PRT; 337 AA.
 AC Q7NHT5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glr250 protein.
 GN OrderedLocustNames=g1r2450;
 OS Gloeobacter violaceus.
 OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.
 OX NCBI_TaxID=33072;
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=PCC 7421;
 RC MEDLINE=22977040; PubMed=14621292;
 RX Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
 Sasamoto S., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,
 Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,
 Takeuchi C., Yamada M., Tabata S.;
 RA "Complete genome structure of Gloeobacter violaceus PCC 7421, a
 cyanobacterium that lacks thylakoids.";
 RT DNA Res. 10:137-145(2003).
 RL EMBL: BA000045; BAC90391.1; -; Genomic_DNA.
 DR HSP: P4169; IOR.
 DR GO: GO:0003824; F:catalytic activity; IEA.
 DR GO: GO:0051287; F:NAD binding; IEA.
 DR GO: GO:0009225; P:nucleotide-sugar metabolism; IEA.
 DR InterPro: IPR001509; Epimerase_Dh.
 DR Pfam: PF01370; Epimerase; 1.
 KW Complete proteome.

SQ SEQUENCE 337 AA; 36521 MW; 3C1B295585AEC94F CRC64;

Query Match 1.0%; Score 9; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 GAKFVQGD1 841
 DB 57 GAKFVQGD1 65

RESULT 12
 Q6W3N9_9PROT PRELIMINARY; PRT; 475 AA.
 AC Q6W3N9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE UDP-murNac-pentapeptide presynthetase.
 GN Name=murF;
 OS *Alvinella pompejana* epibiont 6C6.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria.
 OX NCBI_TaxID=244799;

RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22837667; PubMed=12957888;
 RX DOI=10.1128/AEM.69.9.5070-5078.2003;
 RA Campbell B.J., Stein J.L., Cary S.C.;
 RT "Evidence of chemolithoautotrophy in the bacterial community
 associated with *Alvinella pompejana*, a hydrothermal vent polychaete.";
 RL Appl. Environ. Microbiol. 69:5070-5078(2003).
 DR EMBL: AY312990; AAQ75142.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0009258; P:biosynthesis; IEA.
 DR InterPro: IPR004101; Mur_ligase_C.
 DR InterPro: IPR012237; UDP-NacM_Alig.
 DR Pfam: PF02875; Mur_ligase_C; 1.
 DR PIRSF: PIRSF001562; UDP-NacM_Alig; 1.

SQ SEQUENCE 475 AA; 54554 MW; B6F5F2301CAFLCDD CRC64;
 Query Match 1.0%; Score 9; DB 2; Length 475;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 32 DDFRNGNID 40
 |||||
 Db 369 DDFRNGNID 377
 RESULT 13
 YMA2_YEAST STANDARD; PRT; 737 AA.
 ID YMA2_YEAST
 AC Q04263; Q03665;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Hypothetical 84.6 kDa protein in GLO1-IPF7 intergenic region.
 GN OrderedLocustNames=YML002W; ORFNames=YM9571.17, YM8270.01;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288c / AB972;
 RX MEDLINE=97313268; PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S.V., Whitehead S., Barrett B.G., "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.".
 RT Nature 387:90-93(1997).
 RL
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC
 CC EMBL; Z49810; CAA89950.1; -; Genomic_DNA.
 DR EMBL; Z49810; CAA89950.1; -; Genomic_DNA.
 DR PIR; S55117; S55117.
 DR GenOnline; 142532; -;
 DR Ensembl; YML002W; Saccharomyces cerevisiae.
 DR SGD; S000004461; YML002W.
 DR InterPro; IPR002110; ANK.
 DR SMART; SM00248; ANK; 3.
 DR KMW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 737 AA; 84602 MW; 563B6BA073657C CRC64;
 Query Match 1.0%; Score 9; DB 1; Length 737;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 FSNSSSTK 191
 |||||
 Db 48 FSNSSSTK 56
 RESULT 14
 O6B2L5_YEAST PRELIMINARY; PRT; 737 AA.
 ID O6B2L5_YEAST
 AC O6B2L5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE YML002W.
 GN ORFNames=YML002W;
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Marschall G., Rolfs A., Richardson A., Kane M., Baqui M., Teycher E., Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F., RA Zuo D., Raphael J., Hogle C., Jepson D., Williams J., Camargo A., RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E., RA Labaer J.;
 RT "Creation of the YFLEX clone resource: cloning of Saccharomyces RT cerevisiae ORFs in the Gateway recombinational cloning system."; RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY92715; AY92734.1; -; Genomic_DNA.
 DR Ensembl; YML002W; Saccharomyces cerevisiae.
 DR SGD; S000004461; YML002W.
 DR InterPro; IPR002110; ANK.
 SQ SEQUENCE 737 AA; 84533 MW; 4592E329948375B3 CRC64;
 Query Match 1.0%; Score 9; DB 2; Length 737;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 FSNSSSTK 191
 |||||
 Db 48 FSNSSSTK 56
 RESULT 15
 O823X4_CHLVCV
 ID O823X4_CHLVCV PRELIMINARY; PRT; 868 AA.
 AC O823X4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Polymorphic outer membrane protein G family protein.
 GN OrderedLocustNames=CCA00279;
 OS Chlamydia caviae.
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 CX NCBI_TaxID=33557;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GPIC;
 RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., RA Heidelberg J.F., Holtzapfe B.K., Khouri H.M., Federova N.B., RA Carcy H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J., RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., RA Bayool P.M., Fraser C.M.;
 RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC): RT examining the role of niche-specific genes in the evolution of the RT Chlamydiaceae.";
 RL Nucleic Acids Res. 31:2134-2147(2003).
 DR EMBL; AE016995; AAP05030.1; -; Genomic_DNA.
 DR TIGR; CCA00279; -;
 DR GO; GO:0019867; C:outer membrane, IEA.
 DR InterPro; IPR005546; Auto_transpcbeta.
 DR InterPro; IPR011427; ChlamPMP_M.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autoporter; 1.
 DR Pfam; PF07548; ChlamPMP_M; 1.
 DR Pfam; PF02415; Chlam_PMP; 3.
 DR TIGRFAMs; TIGR01376; POMP_repeat; 1.
 DR Complete proteome.
 SQ SEQUENCE 868 AA; 96015 MW; 52918F69F4FD3FP4 CRC64;
 Query Match 1.0%; Score 9; DB 2; Length 868;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 653 GFRITSGY 661
 |||||
 Db 592 GFRITSGY 600

Mon Nov 28 09:39:52 2005

us-09-446-677b-2.011.rup

Page 7

Search completed: November 25, 2005, 14:46:24
Job time : 144.29 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:24:03 ; Search time 27.6938 Seconds
(without alignments)
2770.401 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 928

Sequence: 1 MKTSLPWLVSIVLAFSCHL.....MELRGSSRNVDVGTGRF 928

Scoring table: OLIGO

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5.COMB.pep:*
2: /cgn2_6/prodata/1/aa/6.COMB.pep:*
3: /cgn2_6/prodata/1/aa/H.COMB.pep:*
4: /cgn2_6/prodata/1/aa/PCTUS.COMB.pep:*
5: /cgn2_6/prodata/1/aa/RS.COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	928	100.0	967	2 US-09-438-185A-453	Sequence 453, App
2	827	89.1	949	2 US-09-198-452A-478	Sequence 478, App
3	12	1.3	230	2 US-09-198-452A-30	Sequence 30, App1
4	12	1.3	780	2 US-09-438-185A-17	Sequence 17, App1
5	12	1.3	928	2 US-09-428-122-2	Sequence 2, App1
6	10	1.1	450	2 US-09-198-452A-35	Sequence 35, App1
7	10	1.1	450	2 US-09-438-185A-21	Sequence 21, App
8	9	1.0	930	2 US-09-198-452A-470	Sequence 470, App
9	9	1.0	938	2 US-09-438-185A-448	Sequence 448, App
10	9	0.9	76	2 US-09-583-110-4935	Sequence 4935, App
11	8	0.9	76	2 US-09-107-433-3629	Sequence 3629, App
12	8	0.9	117	2 US-09-270-767-57096	Sequence 57096, App
13	8	0.9	199	2 US-09-540-236-3194	Sequence 3194, App
14	8	0.9	201	2 US-09-270-767-33568	Sequence 33568, App
15	8	0.9	201	2 US-09-270-767-33568	Sequence 48785, App
16	8	0.9	218	2 US-09-249-180-6	Sequence 6, App1
17	8	0.9	295	2 US-09-248-796A-14734	Sequence 14734, App
18	8	0.9	335	2 US-09-270-767-41852	Sequence 41852, App
19	8	0.9	335	2 US-09-248-796A-14735	Sequence 14735, App
20	8	0.9	427	2 US-09-198-452A-31	Sequence 31, App1
21	8	0.9	458	2 US-09-612-402B-36	Sequence 36, App1
22	8	0.9	458	2 US-09-542-520-36	Sequence 36, App1
23	8	0.9	505	2 US-09-612-402B-17	Sequence 17, App1
24	8	0.9	505	2 US-09-542-520-17	Sequence 17, App1
25	8	0.9	532	2 US-09-198-452A-480	Sequence 480, App
26	8	0.9	530	2 US-09-198-452A-482	Sequence 482, App
27	8	0.9	597	2 US-09-198-452A-29	Sequence 29, App1

28	8	0.9	602	2 US-09-438-185A-18	Sequence 18, App1
29	8	0.9	634	2 US-09-438-185A-451	Sequence 451, App
30	8	0.9	643	2 US-09-198-452A-474	Sequence 474, App
31	8	0.9	670	2 US-10-197-220-169	Sequence 169, App
32	8	0.9	922	2 US-09-198-452A-15	Sequence 15, App1
33	8	0.9	932	2 US-09-438-185A-6	Sequence 6, App1
34	8	0.9	973	2 US-09-430-723-2	Sequence 2, App1
35	8	0.9	982	2 US-09-556-877-176	Sequence 176, App
36	8	0.9	982	2 US-09-620-412C-176	Sequence 176, App
37	8	0.9	982	2 US-09-598-419-176	Sequence 176, App
38	8	0.9	984	2 US-09-612-402B-43	Sequence 43, App1
39	8	0.9	999	2 US-09-438-185A-455	Sequence 455, App
40	8	0.9	1006	2 US-09-556-877-190	Sequence 190, App
41	8	0.9	1006	2 US-09-620-412C-190	Sequence 190, App
42	8	0.9	1006	2 US-09-598-419-190	Sequence 190, App
43	8	0.9	1012	2 US-09-612-402B-2	Sequence 2, App1
44	8	0.9	1012	2 US-09-542-520-2	Sequence 2, App1
45	8	0.9	1013	2 US-09-612-402B-15	Sequence 15, App1

ALIGNMENTS

```
RESULT 1
US-09-438-185A-453
; Sequence 453, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438, 185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108, 279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128, 606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0451
US-09-438-185A-453
Query Match 100.0%; Score 928; DB 2; Length 967;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKTSLPWLVSIVLAFSCHLQSLANEELSPDSEFNGNIDSGTFPEPKTSATYSLTGDYF 60
40 MKTSLPWLVSIVLAFSCHLQSLANEELSPDSEFNGNIDSGTFPEPKTSATYSLTGDYF 99
61 FPEPKGTPLSGSCFKQTTDNLTFNGHSLTFEGFDAGTHAGAASTANKXLPFGSFS 120
100 FPEPKGTPLSGSCFKQTTDNLTFNGHSLTFEGFDAGTHAGAASTANKXLPFGSFS 159
121 LSPSSPSTYTTGGTSLSSAGVNLRIKLVVAGNSTADGAIKASFLTGTSD 180
160 LSPSSPSTYTTGGTSLSSAGVNLRIKLVVAGNSTADGAIKASFLTGTSD 219
181 ALFSSNNSSTKGAATATTAGARIANNNTGYVRLSNIASTSGAIDDEGTSILSNKFLYF 240
220 ALFSSNNSSTKGAATATTAGARIANNNTGYVRLSNIASTSGAIDDEGTSILSNKFLYF 279
241 EGNAAKTGCAICNTKASGPELIIISNNKTLIPASVNAFTSGAIIAKKLAISGGFTTF 300
```

Dh 280 EGNAAKTTGGAICNTKASGPELIIISNNKTLIFASVAETSGAIIHAKKULALSSGGFTTEF 339
Qy 301 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKRNAINISNGK 360
Db 340 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKRNAINISNGK 399
Qy 361 FTBLRAKKNHTTIFPYDPTISEGTSADVAKINNGSAGALNPYQGTILFSGETLTADBLKVA 420
Db 400 FTBLRAKKNHTTIFPYDPTISEGTSADVAKINNGSAGALNPYQGTILFSGETLTADBLKVA 459
Qy 421 DNKSSFTQPVSLSGKLLQKGVLTSETSFSGAGSLGMDSGTTLSTAAGSTTTNIG 480
Db 460 DNKSSFTQPVSLSGKLLQKGVLTSETSFSGAGSLGMDSGTTLSTAAGSTTTNIG 519
Qy 481 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
Db 520 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 579
Qy 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 600
Db 580 VDTNVDISSLIPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 639
Qy 601 ALVNTLMGVPTDRLSLQQLVEIGATGMEHKQGFWSMTNFIHKTGDENRKGFRHTSGG 660
Db 640 ALVNTLMGVPTDRLSLQQLVEIGATGMEHKQGFWSMTNFIHKTGDENRKGFRHTSGG 699
Qy 661 YVIGSAHTPKDDLTFAFCHLFAKDCCFIANNNSRTYGGTLFFKHSHTLQPNYLRLG 720
Db 700 YVIGSAHTPKDDLTFAFCHLFAKDCCFIANNNSRTYGGTLFFKHSHTLQPNYLRLG 759
Qy 721 RAKFESAIIEKPREIPLADVOVSFSHSDNRMETHTYSLPESGWSNCEIAGIGLDL 780
Db 760 RAKFESAIIEKPREIPLADVOVSFSHSDNRMETHTYSLPESGWSNCEIAGIGLDL 819
Qy 781 PFLVSNHPLFKFTIPQMKEMVYVSONSFESSSDRGSGISGRLLNLSTIPVGAKEFVQGD 840
Db 820 PFLVSNHPLFKFTIPQMKEMVYVSONSFESSSDRGSGISGRLLNLSTIPVGAKEFVQGD 879
Qy 841 IGDSTYDLSGFFVSDVYRNPOSTATLVMSPDWMKIRGMLSRQAFLLRGSNNYYVNSN 900
Db 880 IGDSTYDLSGFFVSDVYRNPOSTATLVMSPDWMKIRGMLSRQAFLLRGSNNYYVNSN 939
Qy 901 CELFGHYAMELRGSSRRYNDVGTCLRF 928
Db 940 CELFGHYAMELRGSSRRYNDVGTCLRF 967

RESULT 2

US-09-198-452A-478
; Sequence 478, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 478
; LENGTH: 949
; TYPE: PRN
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...949
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-478

Query Match 89.1%; Score 827; DB 2; Length 949;
Best Local Similarity 99.9%; Fred. No. 0;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKTISPMVLVSSVLAESCHLQSLANBELLSPPDSFNGNIDSGFTTPKTSATTVSLTGDFV 60
Db 22 MKTISPMVLVSSVLAESCHLQSLANBELLSPPDSFNGNIDSGFTTPKTSATTVSLTGDFV 81
Qy 61 FYEPGKGTPLSDSCFQQTDDNLTFLNGHSLTFPGFIDACTHGAASSTANKRLTFSGFS 120
Db 82 FYEPGKGTPLSDSCFQQTDDNLTFLNGHSLTFPGFIDACTHGAASSTANKRLTFSGFS 141
Qy 121 LLSFDSSTTVYTGQGLSSAGVNLNIRKLVAGNSTADGCAIKGASFLITGSD 180
Db 142 LLSFDSSTTVYTGQGLSSAGVNLNIRKLVAGNSTADGCAIKGASFLITGSD 201
Qy 181 ALFSNNSSSTKGAIAITTAGARIANNTRYVRLSNIASTSGAIDDEGTSIISNNKFLYF 240
Db 202 ALFSNNSSSTKGAIAITTAGARIANNTRYVRLSNIASTSGAIDDEGTSIISNNKFLYF 261
Qy 241 EGNAAKTTGGAICNTKASGPELIIISNNKTLIFASVAETSGAIIHAKKULALSSGGFTTEF 300
Db 262 EGNAAKTTGGAICNTKASGPELIIISNNKTLIFASVAETSGAIIHAKKULALSSGGFTTEF 321
Qy 301 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKRNAINISNGK 360
Db 322 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKRNAINISNGK 381
Qy 361 FTBLRAKKNHTTIFPYDPTISEGTSADVAKINNGSAGALNPYQGTILFSGETLTADBLKVA 420
Db 382 FTBLRAKKNHTTIFPYDPTISEGTSADVAKINNGSAGALNPYQGTILFSGETLTADBLKVA 441
Qy 421 DNKSSFTQPVSLSGKLLQKGVLTSETSFSGAGSLGMDSGTTLSTAAGSTTTNIG 480
Db 442 DNKSSFTQPVSLSGKLLQKGVLTSETSFSGAGSLGMDSGTTLSTAAGSTTTNIG 501
Qy 481 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540
Db 502 INVDLGLKQPVSLTAKGASNKVIIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 561
Qy 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 600
Db 562 VDTNVDISSLIPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 621
Qy 601 ALVNTLMGVPTDRLSLQQLVEIGATGMEHKQGFWSMTNFIHKTGDENRKGFRHTSGG 660
Db 622 ALVNTLMGVPTDRLSLQQLVEIGATGMEHKQGFWSMTNFIHKTGDENRKGFRHTSGG 681
Qy 661 YVIGSAHTPKDDLTFAFCHLFAKDCCFIANNNSRTYGGTLFFKHSHTLQPNYLRLG 720
Db 682 YVIGSAHTPKDDLTFAFCHLFAKDCCFIANNNSRTYGGTLFFKHSHTLQPNYLRLG 741
Qy 721 RAKFESAIIEKPREIPLADVOVSFSHSDNRMETHTYSLPESGWSNCEIAGIGLDL 780
Db 742 RAKFESAIIEKPREIPLADVOVSFSHSDNRMETHTYSLPESGWSNCEIAGIGLDL 801
Qy 781 PFLVSNHPLFKFTIPQMKEMVYVSONSFESSSDRGSGISGRLLNLSTIPVGAKEFVQGD 840
Db 802 PFLVSNHPLFKFTIPQMKEMVYVSONSFESSSDRGSGISGRLLNLSTIPVGAKEFVQGD 861
Qy 841 IGDSTYDLSGFFVSDVYRNPOSTATLVMSPDWMKIRGMLSRQAFLLRGSNNYYVNSN 900
Db 862 IGDSTYDLSGFFVSDVYRNPOSTATLVMSPDWMKIRGMLSRQAFLLRGSNNYYVNSN 921
Qy 901 CELFGHYAMELRGSSRRYNDVGTCLRF 928
Db 922 CELFGHYAMELRGSSRRYNDVGTCLRF 949

RESULT 3

US-09-198-452A-30
; Sequence 30, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

```
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 30
; LENGTH: 230
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-30

Query Match
Best Local Similarity 1.3%; Score 12; DB 2; Length 230;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921
Db 212 ELRGSSRNRYND 223

RESULT 4
US-09-438-185A-17
; Sequence 17, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 780
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0015
; US-09-438-185A-17

Query Match
Best Local Similarity 1.3%; Score 12; DB 2; Length 780;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921
Db 762 ELRGSSRNRYND 773

RESULT 5
US-09-428-122-2
; Sequence 2, Application US/09428122
; Patent No. 6872814
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
```

```
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; US-09-428-122-2

Query Match
Best Local Similarity 1.3%; Score 12; DB 2; Length 928;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921
Db 910 ELRGSSRNRYND 921

RESULT 6
US-09-198-452A-35
; Sequence 35, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 35
; LENGTH: 450
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-35

Query Match
Best Local Similarity 1.1%; Score 10; DB 2; Length 450;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYN 919
Db 432 ELRGSSRNRYN 441

RESULT 7
US-09-438-185A-21
; Sequence 21, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 450
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0019
; US-09-438-185A-21
```

Query Match 1.1%; Score 10; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 910 ELRGSSRNRYN 919
|||||
Db 432 ELRGSSRNRYN 441

RESULT 8

US-09-198-452A-470
; Sequence 470, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-470

Query Match 1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 AGAASTTA 110
|||||
Db 107 AGAASTTA 115

RESULT 9

US-09-438-185A-448
; Sequence 448, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 448
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0446
US-09-438-185A-448

Query Match 1.0%; Score 9; DB 2; Length 938;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 AGAASTTA 110
|||||
Db 115 AGAASTTA 123

RESULT 10
US-09-583-110-4935
; Sequence 4935, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucet-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnosis and Therapeutics
; FILE REFERENCE: PAT00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4935
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4935

Query Match 0.9%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 412 LTADELKV 419
|||||
Db 25 LTADELKV 32

RESULT 11

US-09-107-433-3629
; Sequence 3629, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucet-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3629:


```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 76 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Streptococcus pneumoniae
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...76
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3629:
US-09-107-433-3629

Query Match
Best Local Similarity 100.0%; DB 2; Length 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 LTADELKV 419
Db 25 LTADELKV 32

RESULT 12
US-09-270-767-57096
; Sequence 57096, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 57096
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57096

Query Match
Best Local Similarity 100.0%; DB 2; Length 117;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 NAAKTGG 250
Db 4 NAAKTGG 11

RESULT 13
US-09-540-236-3194
; Sequence 3194, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;   APPLICANT: Gary L. Breton et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATRA
;   FILE REFERENCE: 2709.2005-001
;   CURRENT APPLICATION NUMBER: US/09/540,236
;   CURRENT FILING DATE: 2000-04-04
;   NUMBER OF SEQ ID NOS: 3840
;   SEQ ID NO 3194
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: M.catarhalis
US-09-540-236-3194

Query Match
Best Local Similarity 100.0%; DB 2; Length 199;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 744 VFSHSDN 751
Db 83 VFSHSDN 90

RESULT 14
US-09-270-767-33568
; Sequence 33568, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 33568
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-33568

Query Match
Best Local Similarity 100.0%; DB 2; Length 201;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAASTTA 110
Db 143 GAASTTA 150

RESULT 15
US-09-270-767-48785
; Sequence 48785, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 48785
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-48785

Query Match
Best Local Similarity 100.0%; DB 2; Length 201;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAASTTA 110
Db 143 GAASTTA 150

Search completed: November 25, 2005, 14:49:57
Job time : 28.6938 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:30:28 ; Search time 97.9541 Seconds

(without alignments)
3958.441 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 928
Sequence: 1 MKTSLPWLVSVAFLSFCHL.....MELRGSSRRNYNDVGTGLR 928Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	928	100.0	928	4 US-10-312-273-115	Sequence 115, App
2	928	100.0	928	4 US-10-282-122A-54681	Sequence 54681, A
3	827	89.1	949	4 US-10-289-762-478	Sequence 478, App
4	12	1.3	230	4 US-10-289-762-30	Sequence 30, Appl
5	12	1.3	746	4 US-10-312-273-19	Sequence 19, Appl
6	12	1.3	928	3 US-09-428-122-2	Sequence 2, Appl
7	10	1.1	395	4 US-10-312-273-21	Sequence 21, Appl
8	10	1.1	450	4 US-10-289-762-35	Sequence 35, Appl
9	10	1.1	839	3 US-09-738-262-23	Sequence 23, Appl
10	10	1.1	839	4 US-10-023-437-23	Sequence 23, Appl
11	9	1.0	930	4 US-10-312-273-45	Sequence 45, Appl
12	9	1.0	930	4 US-10-289-762-470	Sequence 470, Appl
13	9	1.0	930	4 US-10-282-122A-54680	Sequence 54680, A
14	8	0.9	53	4 US-10-425-115-353071	Sequence 353071, A
15	8	0.9	76	5 US-10-617-320-3629	Sequence 3629, Ap
16	8	0.9	92	4 US-10-437-963-181650	Sequence 181650, A
17	8	0.9	93	4 US-10-291-265-251	Sequence 251, App
18	8	0.9	93	4 US-10-291-265-723	Sequence 723, App
19	8	0.9	112	4 US-10-106-698-5720	Sequence 5720, Ap
20	8	0.9	140	4 US-10-425-115-272446	Sequence 272446, A
21	8	0.9	171	4 US-10-425-115-255238	Sequence 255238, A
22	8	0.9	218	3 US-09-742-137-6	Sequence 6, Appl
23	8	0.9	218	3 US-09-742-160A-6	Sequence 6, Appl
24	8	0.9	218	4 US-10-310-154-691	Sequence 691, App
25	8	0.9	225	4 US-10-425-115-304034	Sequence 304034, A
26	8	0.9	227	4 US-10-309-804-8	Sequence 8, Appl
27	8	0.9	227	4 US-10-391-399-12	Sequence 12, Appl

28	8	0.9	231	4 US-10-425-115-247895	Sequence 247895, A
29	8	0.9	234	3 US-09-764-875-767	Sequence 767, App
30	8	0.9	240	4 US-10-425-115-271893	Sequence 271893, A
31	8	0.9	267	3 US-09-764-870-358	Sequence 359, App
32	8	0.9	267	4 US-10-125-540-359	Sequence 359, App
33	8	0.9	312	4 US-10-425-115-67993	Sequence 67993, A
34	8	0.9	324	4 US-10-389-566-910	Sequence 910, App
35	8	0.9	342	4 US-10-369-499-2885	Sequence 2825, Ap
36	8	0.9	427	4 US-10-289-762-31	Sequence 31, Appl
37	8	0.9	428	4 US-10-437-963-179295	Sequence 179295, A
38	8	0.9	432	5 US-10-873-467-60	Sequence 60, Appl
39	8	0.9	456	4 US-10-112-944-329	Sequence 329, App
40	8	0.9	458	4 US-10-701-844-36	Sequence 36, Appl
41	8	0.9	458	4 US-10-766-711-36	Sequence 36, Appl
42	8	0.9	458	5 US-10-931-776-36	Sequence 36, Appl
43	8	0.9	486	3 US-09-738-628-5629	Sequence 5629, Ap
44	8	0.9	499	5 US-10-739-930-8216	Sequence 8216, Ap
45	8	0.9	505	4 US-10-701-844-17	Sequence 17, Appl

ALIGNMENTS

Result 1

US-10-312-273-115

Sequence 115, Application US/10312273

Publication No. US2004000567A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

FILE REFERENCE: P025035WO

CURRENT APPLICATION NUMBER: US/10/312,273

CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: 0016363.4

PRIOR FILING DATE: 2000-07-03

PRIOR APPLICATION NUMBER: 0017047.2

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 0017983.8

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 0019368.0

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 0020440.4

PRIOR FILING DATE: 2000-08-18

PRIOR APPLICATION NUMBER: 0022583.9

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 0027549.5

PRIOR FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 0031706.5

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 664

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 115

LENGTH: 928

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

US-10-312-273-115

Query Match 100.0%; Score 928; DB 4; Length 928;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKTSLPWLVSVAFLSFCHLQSLANEELSPDSENGNIDSTFPKPSATYSLTGDF	60
DB	1	MKTSLPWLVSVAFLSFCHLQSLANEELSPDSENGNIDSTFPKPSATYSLTGDF	60
QY	61	FYEPKGPPLSDSCKOTTDNLPLNGHSLTFPGIDAGTAGAATSTANKLTFSGRS	120
DB	61	FYEPKGPPLSDSCKOTTDNLPLNGHSLTFPGIDAGTAGAATSTANKLTFSGRS	120
QY	121	LSPFSSSTVTYTGQGLTSSAGGVNLENIRKLVAAGNFSTADGAIKGSFLLTGTSGD	180
DB	121	LSPFSSSTVTYTGQGLTSSAGGVNLENIRKLVAAGNFSTADGAIKGSFLLTGTSGD	180

```
QY 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFLSNIASTSGAIDDEGTSILSNKFLYF 240
| | | | |
DB 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
| | | | |
DB 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
QY 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVNTLTGTSSTDPKRNAINIGSNGK 360
| | | | |
DB 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVNTLTGTSSTDPKRNAINIGSNGK 360
QY 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
| | | | |
DB 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
| | | | |
DB 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
QY 481 INVDSLGLKQPVSLTAKGASNKYIVSGKMLIDIEGNIYESHMFSDOLFSLKITYDAD 540
| | | | |
DB 481 INVDSLGLKQPVSLTAKGASNKYIVSGKMLIDIEGNIYESHMFSDOLFSLKITYDAD 540
QY 541 VDTNVDISSLIPVPAEDPNSEYGFQOGMNVMTTDTATNTKEATATWTKTGVPSPERKS 600
| | | | |
DB 541 VDTNVDISSLIPVPAEDPNSEYGFQOGMNVMTTDTATNTKEATATWTKTGVPSPERKS 600
QY 601 ALVGNLTMGVFTIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSG 660
| | | | |
DB 601 ALVGNLTMGVFTIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSG 660
QY 661 YVIGSAAHTPKDOLLTFPAFCHLPARDKCFIAHNSHTYGGTLFFKHSHTLQPNYLRLG 720
| | | | |
DB 661 YVIGSAAHTPKDOLLTFPAFCHLPARDKCFIAHNSHTYGGTLFFKHSHTLQPNYLRLG 720
QY 721 RAFFSSSAIEKFPREIPLADVOVSFSHSNRMETHYTSLEBSGSMSNCLAGGIGL 780
| | | | |
DB 721 RAFFSSSAIEKFPREIPLADVOVSFSHSNRMETHYTSLEBSGSMSNCLAGGIGL 780
QY 781 PFLSNPHPLFKTFIPQMKEMYVSGNSFESSSDRGFSIGRLNLSTIPVGAKKFYQGD 840
| | | | |
DB 781 PFLSNPHPLFKTFIPQMKEMYVSGNSFESSSDRGFSIGRLNLSTIPVGAKKFYQGD 840
QY 841 IGDSTYDLSGFFVSDVYRNNPOSTATLVMSPDWSKIRGANLSHQAFLRLGSNNYVNSN 900
| | | | |
DB 841 IGDSTYDLSGFFVSDVYRNNPOSTATLVMSPDWSKIRGANLSHQAFLRLGSNNYVNSN 900
QY 901 CELFGHYAMELRGSSRYNNDVGTCLRF 928
| | | | |
DB 901 CELFGHYAMELRGSSRYNNDVGTCLRF 928

RESULT 2
US-10-282-122A-54681
; Sequence 54681, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Twack, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forstch, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
```

```
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54681
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54681

Query Match 100.0%; Score 928; DB 4; Length 928;
Best Local Similarity 100.0%; Pred No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTISIPWLVSSVLAFCSLQSLANBELLSPPDSFNGNIDSGTFPRTSATYSLTGDF 60
| | | | |
DB 1 MKTISIPWLVSSVLAFCSLQSLANBELLSPPDSFNGNIDSGTFPRTSATYSLTGDF 60
QY 61 FYEPGKGTPLSDSCFPQOTDNLTFLGNGSLTFGFI DACTHGAASTTANKRLTFSGS 120
| | | | |
DB 61 FYEPGKGTPLSDSCFPQOTDNLTFLGNGSLTFGFI DACTHGAASTTANKRLTFSGS 120
QY 121 LLSFDSSEPTTYTGGGTSLSAGVNL ENIRKLVAGNFSADGAIKASFLLTGSGD 180
| | | | |
DB 121 LLSFDSSEPTTYTGGGTSLSAGVNL ENIRKLVAGNFSADGAIKASFLLTGSGD 180
QY 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFLSNIASTSGAIDDEGTSILSNKFLYF 240
| | | | |
DB 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
| | | | |
DB 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
QY 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVNTLTGTSSTDPKRNAINIGSNGK 360
| | | | |
DB 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVNTLTGTSSTDPKRNAINIGSNGK 360
QY 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
| | | | |
DB 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
| | | | |
DB 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
QY 481 INVDSLGLKQPVSLTAKGASNKYIVSGKMLIDIEGNIYESHMFSDOLFSLKITYDAD 540
| | | | |
DB 481 INVDSLGLKQPVSLTAKGASNKYIVSGKMLIDIEGNIYESHMFSDOLFSLKITYDAD 540
QY 541 VDTNVDISSLIPVPAEDPNSEYGFQOGMNVMTTDTATNTKEATATWTKTGVPSPERKS 600
| | | | |
DB 541 VDTNVDISSLIPVPAEDPNSEYGFQOGMNVMTTDTATNTKEATATWTKTGVPSPERKS 600
```

QY 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNKRKGFRTTSG 660
DB 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNKRKGFRTTSG 660
QY 661 YVIGSAHTPKDCLFTPAFCHLPARDKDCFIANNSTRYGGTLFPKGSHTLQPNYLRIG 720
DB 661 YVIGSAHTPKDCLFTPAFCHLPARDKDCFIANNSTRYGGTLFPKGSHTLQPNYLRIG 720
QY 721 RAKFSASAIKPKPREPLALDVQVSFSDNRMETHYSLPESGSMNECIAAGIGLUD 780
DB 721 RAKFSASAIKPKPREPLALDVQVSFSDNRMETHYSLPESGSMNECIAAGIGLUD 780
QY 781 PVLSPHPLFKFTFIPOMKVEWYVSONSPFESSSDGRGFSIGRLNLSIPYGAKEVQGD 840
DB 781 PVLSPHPLFKFTFIPOMKVEWYVSONSPFESSSDGRGFSIGRLNLSIPYGAKEVQGD 840
QY 841 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPSWKIRGNSLRQAFLLRGSNNVYNSN 900
DB 841 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPSWKIRGNSLRQAFLLRGSNNVYNSN 900
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 3

US-10-289-762-478
; Sequence 478, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 478
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...949
; OTHER INFORMATION: Xaa=unknown or other
US-10-289-762-478

Query Match 89.1%; Score 827; DB 4; Length 949;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTISPMVLVSVLAESCHLQSLANBELSPDPSFNGNIDSGTTPKTSATVYSLTGDFV 60
DB 22 MKTISPMVLVSVLAESCHLQSLANBELSPDPSFNGNIDSGTTPKTSATVYSLTGDFV 81
QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLANGSLTGFIDAGTHAAGAASTTANKULTSNGFS 120
DB 82 FYEPGKGTPLSDSCFKQTTDNLTFLANGSLTGFIDAGTHAAGAASTTANKULTSNGFS 141
QY 121 LUSFDSPTTYYTGGTSLSSAGVNLNRLVVGPNFTAGGAIKXGSPFLITGSGD 180
DB 142 LUSFDSPTTYYTGGTSLSSAGVNLNRLVVGPNFTAGGAIKXGSPFLITGSGD 201
QY 181 ALFSNNSSSTKGAIAATTAGARIANNVYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 202 ALFSNNSSSTKGAIAATTAGARIANNVYRFLSNIASTSGAIDDEGTSILSNKFLYF 261
QY 241 EGNAAKTTGAIICNTYASGSPPELLISNNKTLIPASVNAETSGAIIHAKKIALSSGGFTF 300
DB 262 EGNAAKTTGAIICNTYASGSPPELLISNNKTLIPASVNAETSGAIIHAKKIALSSGGFTF 321

QY 301 LRNNVSSATPKGGAISIDASGELSIAETGNITTPVARNLTITTTGSDTTPRRNAINIGSNCK 360
DB 322 LRNNVSSATPKGGAISIDASGELSIAETGNITTPVARNLTITTTGSDTTPRRNAINIGSNCK 381
QY 361 FTELRAAKNHTLFPDPITSEGTSSDVYLKINNAGALNPYGGTLIFSGETTLTADBLKVA 420
DB 382 FTELRAAKNHTLFPDPITSEGTSSDVYLKINNAGALNPYGGTLIFSGETTLTADBLKVA 441
QY 421 DNLKSFTQPVSLSGCKLLQKGVTLSTSPQEAASLIGMDSGTTLSTTAGSITTTNIG 480
DB 442 DNLKSFTQPVSLSGCKLLQKGVTLSTSPQEAASLIGMDSGTTLSTTAGSITTTNIG 501
QY 481 INVDSLGLKQPVSLTAKGANKVIVSGKLNLDIEGNIESHMFSDQLFSLKLTIVDAD 540
DB 502 INVDSLGLKQPVSLTAKGANKVIVSGKLNLDIEGNIESHMFSDQLFSLKLTIVDAD 561
QY 541 VDTNVDISLIVPAEDPNSSEYFGQGMVNWTTDTATNTKATATWTTCGVPSPERKS 600
DB 562 VDTNVDISLIVPAEDPNSSEYFGQGMVNWTTDTATNTKATATWTTCGVPSPERKS 621
QY 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNKRKGFRTTSG 660
DB 622 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNKRKGFRTTSG 681
QY 661 YVIGSAHTPKDCLFTPAFCHLPARDKDCFIANNSTRYGGTLFPKGSHTLQPNYLRIG 720
DB 682 YVIGSAHTPKDCLFTPAFCHLPARDKDCFIANNSTRYGGTLFPKGSHTLQPNYLRIG 741
QY 721 RAKFSASAIKPKPREPLALDVQVSFSDNRMETHYSLPESGSMNECIAAGIGLUD 780
DB 742 RAKFSASAIKPKPREPLALDVQVSFSDNRMETHYSLPESGSMNECIAAGIGLUD 801
QY 781 PVLSPHPLFKFTFIPOMKVEWYVSONSPFESSSDGRGFSIGRLNLSIPYGAKEVQGD 840
DB 802 PVLSPHPLFKFTFIPOMKVEWYVSONSPFESSSDGRGFSIGRLNLSIPYGAKEVQGD 861
QY 841 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPSWKIRGNSLRQAFLLRGSNNVYNSN 900
DB 862 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPSWKIRGNSLRQAFLLRGSNNVYNSN 921
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928
DB 922 CELFGHYAMELRGSSRNRYNDVGTCLRF 949

RESULT 4

US-10-289-762-30
; Sequence 30, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 30
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-30

Query Match 1.3%; Score 12; DB 4; Length 230;

Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSERNYND 921
DB 212 ELRGSERNYND 223

RESULT 5
US-10-312-273-19
; Sequence 19, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/10/312,273
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 19
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-19

Query Match 1.3%; Score 12; DB 4; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 910 ELRGSSRNRYND 921
Db 728 ELRGSSRNRYND 739

RESULT 6
US-09-428-122-2
; Sequence 2, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-428-122-2

Query Match 1.3%; Score 12; DB 3; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 910 ELRGSSRNRYND 921
Db 910 ELRGSSRNRYND 921

Db 910 ELRGSSRNRYND 921

RESULT 7
US-10-312-273-21
; Sequence 21, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/10/312,273
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 21
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-21

Query Match 1.1%; Score 10; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 910 ELRGSSRNRYN 919
Db 377 ELRGSSRNRYN 386

RESULT 8
US-10-289-762-35
; Sequence 35, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 97110-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 35
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-35

Query Match 1.1%; Score 10; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 910 ELRGSSRNRYN 919
Db 432 ELRGSSRNRYN 441

```
RESULT 9
US-09-738-269-23
; Sequence 23, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-23

Query Match
Best Local Similarity 100.0%; Score 10; DB 3; Length 839;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTFLGNG 88
DB 81 TDNLTFLGNG 90

RESULT 10
US-10-023-437-23
; Sequence 23, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS for Vaccination COMPRISING NUCLEIC ACID
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-23

Query Match
Best Local Similarity 100.0%; Score 10; DB 4; Length 839;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTFLGNG 88
DB 81 TDNLTFLGNG 90

RESULT 11
US-10-312-273-45
; Sequence 45, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
```

```
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWIn99, version 1.02
; SEQ ID NO 45
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-45

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 930;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAAASTTA 110
DB 107 AGAAASTTA 115

RESULT 12
US-10-289-762-470
; Sequence 470, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifflair, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-470

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 930;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAAASTTA 110
DB 107 AGAAASTTA 115

RESULT 13
US-10-282-122A-54680
; Sequence 54680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haseibeck, Robert
```


APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54680
LENGTH: 930
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54680

Query Match 1.0%; Score 9; DB 4; Length 930;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 AGAAATTA 110
Db 107 AGAAATTA 115

RESULT 14
US-10-425-115-353071
Sequence 353071, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 353071
LENGTH: 53
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_85171C.1.pep
US-10-425-115-353071

Query Match 0.9%; Score 8; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 669 TPXDDLT 676
Db 42 TPXDDLT 49

RESULT 15
US-10-617-320-3629
Sequence 3629, Application US/10617320
Publication No. US20050136404A1
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3629:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...76
SEQUENCE DESCRIPTION: SEQ ID NO: 3629:
US-10-617-320-3629

Query Match 0.9%; Score 8; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 412 LTADELKV 419
Db 25 LTADELKV 32

Mon Nov 28 09:39:52 2005

us-09-446-677b-2.oli.rapbm

Page 7

Job time : 99.9541 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:37:47 ; Search time 3.58994 Seconds
(without alignments)
783.506 Million cell updates/sec

Title: US-09-446-677b-2

Sequence: 1 MKTSIPWLVSSVLAFFSCHL.....MELRGSSRNVDVGTGRF 928

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 17545 seqs, 3030971 residues

Word size: 7

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications_AA_New:*

- 1: /cgn2_6/pcodata/2/pubppaa/US10_NEW_PUB pep.*
- 2: /cgn2_6/pcodata/2/pubppaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/pcodata/2/pubppaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/pcodata/2/pubppaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/pcodata/2/pubppaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/pcodata/2/pubppaa/US11_NEW_PUB pep.*
- 7: /cgn2_6/pcodata/2/pubppaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/pcodata/2/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	0.8	245	US-11-054-515-1714	Sequence 1714, Ap
2	7	0.8	248	US-11-054-515-895	Sequence 895, App
3	7	0.8	249	US-11-054-515-1142	Sequence 1142, Ap
4	7	0.8	249	US-11-054-515-1204	Sequence 1204, Ap
5	7	0.8	249	US-11-054-515-1205	Sequence 1205, Ap
6	7	0.8	249	US-11-054-515-1215	Sequence 1215, Ap
7	7	0.8	250	US-11-054-515-901	Sequence 901, App
8	7	0.8	250	US-11-054-515-1017	Sequence 1017, Ap
9	7	0.8	250	US-11-054-515-1032	Sequence 1032, Ap
10	7	0.8	250	US-11-054-515-1158	Sequence 1158, Ap
11	7	0.8	250	US-11-054-515-1203	Sequence 1203, Ap
12	7	0.8	250	US-11-054-515-1222	Sequence 1222, Ap
13	7	0.8	250	US-11-054-515-1228	Sequence 1228, Ap
14	7	0.8	250	US-11-054-515-1715	Sequence 1715, App
15	7	0.8	251	US-11-054-515-904	Sequence 904, App
16	7	0.8	251	US-11-054-515-1023	Sequence 1023, Ap
17	7	0.8	251	US-11-054-515-1133	Sequence 1133, Ap
18	7	0.8	251	US-11-054-515-1154	Sequence 1154, Ap
19	7	0.8	251	US-11-054-515-1213	Sequence 1213, Ap
20	7	0.8	251	US-11-054-515-1217	Sequence 1217, Ap
21	7	0.8	251	US-11-054-515-1225	Sequence 1225, Ap
22	7	0.8	251	US-11-054-515-1231	Sequence 1231, Ap
23	7	0.8	251	US-11-054-515-1487	Sequence 1487, Ap
24	7	0.8	251	US-11-054-515-1831	Sequence 1831, Ap
25	7	0.8	252	US-11-054-515-1144	Sequence 1144, Ap

26	7	0.8	252	US-11-054-515-1208	Sequence 1208, Ap
27	7	0.8	253	US-11-054-515-929	Sequence 929, App
28	7	0.8	253	US-11-054-515-935	Sequence 935, App
29	7	0.8	253	US-11-054-515-939	Sequence 939, App
30	7	0.8	308	US-10-793-626-1072	Sequence 1072, Ap
31	7	0.8	308	US-10-793-626-2706	Sequence 2706, Ap
32	7	0.8	394	US-10-793-626-3292	Sequence 3292, Ap
33	7	0.8	417	US-10-858-730-60	Sequence 60, App1
34	7	0.8	3144	US-11-055-035-1	Sequence 1, App1
35	6	0.6	16	US-11-054-515-2907	Sequence 2907, Ap
36	6	0.6	90	US-11-053-076-146	Sequence 146, App
37	6	0.6	92	US-10-689-742-6	Sequence 6, App1
38	6	0.6	92	US-11-053-076-121	Sequence 121, App1
39	6	0.6	124	US-11-040-159-10	Sequence 10, App1
40	6	0.6	142	US-10-789-273-16	Sequence 16, App1
41	6	0.6	142	US-10-821-234-929	Sequence 929, App
42	6	0.6	142	US-10-821-234-1030	Sequence 1030, Ap
43	6	0.6	144	US-10-793-626-1640	Sequence 1640, Ap
44	6	0.6	144	US-10-793-626-1958	Sequence 1958, Ap
45	6	0.6	144	US-11-174-398-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-11-054-515-1714
; Sequence 1714, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blus
; FILE REFERENCE: PFS423P3
; CURRENT APPLICATION NUMBER: US/11/054, 515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543, 296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580, 347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293, 418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331, 469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340, 817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880, 748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293, 499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277, 379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276, 248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240, 816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1714
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1714
Query Match 0.8%; Score 7; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 411 TTAADEL 417
DB 69 TTAADEL 75
RESULT 2

```
US-11-054-515-895
; Sequence 895, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 895
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-895

Query Match      0.8%; Score 7; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      411 TLTDEL 417
      |||||
Db      68 TLTDEL 74

RESULT 3
US-11-054-515-1142
; Sequence 1142, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 895
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-895
```

```
US-11-054-515-1204
; Sequence 1204, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1204
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1204

Query Match      0.8%; Score 7; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      411 TLTDEL 417
      |||||
Db      69 TLTDEL 75

RESULT 5
US-11-054-515-1205
; Sequence 1205, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1204
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1204
```

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1205
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1205

Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 249;
Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 TTFADEL 417
|||||
Db 69 TTFADEL 75

RESULT 6
US-11-054-515-1215
Sequence 1215, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1215
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1215

Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 249;
Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 TTFADEL 417
|||||
Db 69 TTFADEL 75

RESULT 7
US-11-054-515-901
Sequence 901, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 901
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-901

Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 250;
Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 TTFADEL 417
|||||
Db 69 TTFADEL 75

RESULT 8
US-11-054-515-1017
Sequence 1017, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296

```
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1017
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1017
```

```
Query Match          0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      411 TLTDEL 417
         |||||
Db       69 TLTDEL 75
```

RESULT 9

```
US-11-054-515-1022
; Sequence 1022, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PF523P3
```

```
; CURRENT APPLICATION NUMBER: US/11/054,515
```

```
; PRIOR FILING DATE: 2005-02-10
```

```
; PRIOR APPLICATION NUMBER: 60/543,296
```

```
; PRIOR FILING DATE: 2004-02-11
```

```
; PRIOR APPLICATION NUMBER: 60/580,347
```

```
; PRIOR FILING DATE: 2004-06-18
```

```
; PRIOR APPLICATION NUMBER: 10/293,418
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/331,469
```

```
; PRIOR FILING DATE: 2001-11-16
```

```
; PRIOR APPLICATION NUMBER: 60/340,817
```

```
; PRIOR FILING DATE: 2001-12-19
```

```
; PRIOR APPLICATION NUMBER: 09/880,748
```

```
; PRIOR FILING DATE: 2001-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/293,499
```

```
; PRIOR FILING DATE: 2001-05-25
```

```
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
```

```
; PRIOR APPLICATION NUMBER: 60/276,248
```

```
; PRIOR FILING DATE: 2001-03-16
```

```
; PRIOR APPLICATION NUMBER: 60/240,816
```

```
; PRIOR FILING DATE: 2000-10-17
```

```
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 3247
```

```
; SEQ ID NO 1022
```

```
; LENGTH: 250
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-11-054-515-1022
```

```
Query Match          0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      411 TLTDEL 417
         |||||
Db       69 TLTDEL 75
```

RESULT 10

```
US-11-054-515-1158
; Sequence 1158, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PF523P3
```

```
; CURRENT APPLICATION NUMBER: US/11/054,515
```

```
; PRIOR FILING DATE: 2005-02-10
```

```
; PRIOR APPLICATION NUMBER: 60/543,296
```

```
; PRIOR FILING DATE: 2004-02-11
```

```
; PRIOR APPLICATION NUMBER: 60/580,347
```

```
; PRIOR FILING DATE: 2004-06-18
```

```
; PRIOR APPLICATION NUMBER: 10/293,418
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/331,469
```

```
; PRIOR FILING DATE: 2001-11-16
```

```
; PRIOR APPLICATION NUMBER: 60/340,817
```

```
; PRIOR FILING DATE: 2001-12-19
```

```
; PRIOR APPLICATION NUMBER: 09/880,748
```

```
; PRIOR FILING DATE: 2001-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/293,499
```

```
; PRIOR FILING DATE: 2001-05-25
```

```
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
```

```
; PRIOR APPLICATION NUMBER: 60/276,248
```

```
; PRIOR FILING DATE: 2001-03-16
```

```
; PRIOR APPLICATION NUMBER: 60/240,816
```

```
; PRIOR FILING DATE: 2000-10-17
```

```
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 3247
```

```
; SEQ ID NO 1158
```

```
; LENGTH: 250
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-11-054-515-1158
```

```
Query Match          0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      411 TLTDEL 417
         |||||
Db       69 TLTDEL 75
```

RESULT 11

```
US-11-054-515-1203
; Sequence 1203, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PF523P3
```

```
; CURRENT APPLICATION NUMBER: US/11/054,515
```

```
; PRIOR FILING DATE: 2005-02-10
```

```
; PRIOR APPLICATION NUMBER: 60/543,296
```

```
; PRIOR FILING DATE: 2004-02-11
```

```
; PRIOR APPLICATION NUMBER: 60/580,347
```

```
; PRIOR FILING DATE: 2004-06-18
```

```
; PRIOR APPLICATION NUMBER: 10/293,418
```

```
; PRIOR FILING DATE: 2002-11-14
```



```

; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1203
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1203
```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      411 TLTADEL 417
Db      69 TLTADEL 75
```

```

RESULT 12
US-11-054-515-1222
; Sequence 1222, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1222
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1222
```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      411 TLTADEL 417
Db      69 TLTADEL 75
```

```

RESULT 13
US-11-054-515-1228
; Sequence 1228, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1228
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1228
```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      411 TLTADEL 417
Db      69 TLTADEL 75
```

```

RESULT 14
US-11-054-515-1715
; Sequence 1715, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
```

Search completed: November 25, 2005, 14:56:47
Job time : 4.83994 secs

```

; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1715
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1715

```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      411 TLTADEL 417
Db      69 TLTADEL 75

```

```

RESULT 15
US-11-054-515-904
; Sequence 904, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 904
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-904

```

```

Query Match      0.8%; Score 7; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      411 TLTADEL 417
Db      69 TLTADEL 75

```

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)